

Query Match	100 0%	Score 1772;	DB 4;	Length 1772;				
Best Local Similarity	100 0%	Pred. No. 0;	Mismatches 0;	Indels 0;	Gaps 0;			
Matches 1772; Conservative 0;								
Qy	1	ACTTGTAGATAAAGTAAGTCAGAGAAATAATAATTCAATTTTTAAATA 60						
Db	1	ACTTGTAGATAAAGTAAGTCAGAGAAATAATAATTCAATTTTTAAATA 60						
Qy	61	AGACGAGTGGTCAAACAGTAGAAGCTAAATCCTTATATTGGACTTATA 120						
Db	61	AGACGAGTGGTCAAACAGTAGAAGCTAAATCCTTATATTGGACTTATA 120						
Qy	121	TTATGGCGAGGAGTAGGAGTAGGAGATGTAGCCAGAAAACACACCGC 180						
Db	121	TTATGGCGAGGAGTAGGAGATGTAGCCAGAAAACACACACCGC 180						
Qy	181	CACCTGGCAGGCATGGCATCTAGGTCGACATTGGAGGCTGGCAGTAGCAGT 240						
Db	181	CACCTGGCAGGCATGGCATCTAGGTCGACATTGGAGGCTGGCAGTAGCAGT 240						
Qy	241	CTACACACATGCTTCAGTCAGCTAGCTAGCTAGCTACATTCAGGG 300						
Db	241	CTACACACATGCTTCAGTCAGCTAGCTAGCTACATTCAGGG 300						
Qy	301	CAGCAGTAGGCAACAGCTTGAGGAAACAATCGATAATCGATTTGTCAAGGAGAACATG 360						
Db	301	CAGCAGTAGGCAACAGCTTGAGGAAACAATCGATAATCGATTTGTCAAGGAGAACATG 360						
Qy	361	GAGAAAAACCGGGCTCGAGAGAACCGAGCTAACCTCAACTGGCTCTGAAGGGCTGA 420						
Db	361	GAGAAAAACCGGGCTCGAGAGAACCGAGCTAACCTCAACTGGCTCTGAAGGGCTGA 420						
Qy	421	ACCCATCTGCAAATCGAGATTGGTTGTTCAATTCTGAACTTCTCAGATG 480						
Db	421	ACCCATCTGCAAATCGAGATTGGTTGTTCAATTCTGAACTTCTCAGATG 480						
Qy	481	GTTCGATGTTCAACCGTAGTACATCTGAAAATGAAGTGTAAATACTCTGAGAACACT 540						
Db	481	GTTCGATGTTCAACCGTAGTACATCTGAAAATGAAGTGTAAATACTCTGAGAACACT 540						
Qy	541	TCTATGGAAAGCATGCCCTGAGCGATTAGCTAAGAAAAAAATAATGTACTTTTTCGAA 600						
Db	541	TCTATGGAAAGCATGCCCTGAGCGATTAGCTAAGAAAAAAATAATGTACTTTTTCGAA 600						
Qy	601	ACTTAATTGCGAGTAAATGCGATATAAAATTATCGATGTTAAATCTTCAAGTCA 660						
Db	601	ACTTAATTGCGAGTAAATGCGATATAAAATTATCGATGTTAAATCTTCAAGTCA 660						
Qy	661	GTTTAAACCGTAAATGCGATATAAAATTATCGATGTTAAATCTTCAAGTCA 720						
Db	661	GTTTAAACCGTAAATGCGATATAAAATTATCGATGTTAAATCTTCAAGTCA 720						
Qy	721	TAGTTGCTTCGTTCAATTCTPACCCTTCAACCATAGCTCAATTGCAAA 780						
Db	721	TAGTTGCTTCGTTCAATTCTPACCCTTCAACCATAGCTCAATTGCAAA 780						
Qy	781	TAAAAGTTACTAACGAGAACATCGCTCATACACACCCAAAGCTCACCCATGGCTCCTC 840						
Db	781	TAAAAGTTACTAACGAGAACATCGCTCATACACCCAAAGCTCACCCATGGCTCCTC 840						
Qy	841	GACCAAGGTTAGACTGTGAACTATATCGTGGATGAAACATACATGCGCC 900						
Db	841	GACCAAGGTTAGACTGTGAACTATATCGTGGATGAAACATACATGCGCC 900						
Qy	901	ATGCCGAATTAGGGCTCTCATGACCTTCAACGGCACAGGGTGAAGGAT 960						
Db	901	ATGCCGAATTAGGGCTCTCATGACCTTCAACGGCACAGGGTGAAGGAT 960						
Qy	961	GCATGCTATGCCCTCTGTGAAAGAACAAAGTTACTGGTAAATGACATGCTGTAGCT 1020						
Db	961	GCATGCTATGCCCTCTGTGAAAGAACAAAGTTACTGGTAAATGACATGCTGTAGCT 1020						
Qy								
Db								
RESULT 2								
ID	AAP24787	standard; DNA; 1803 BP.						
XX								
AC	AAP24787;							
XX								
DT	20-APR-2001	(first entry)						
XX								
DE	Nucleotide sequence of a rice sucrose synthase 3 (RSuS3) promoter.							
XX								
KW	Rice; sucrose synthase 3 promoter; RSuS3 promoter; endosperm expression; transgenic plant; carbohydrate metabolism; sucrose metabolism; 66.							
XX								
OS	Oryza sativa.							
XX								
PN	WO200078975-A2.							
XX								
PD	28-DEC-2000.							
XX								
PF	15-JUN-2000; 2000WO-GB002641.							

QY	1741	TAGAGTTCCCTCTTCACTGCAG	1772		241	CTACACAACTGCTTCACTGAGCTTCACTGCATGTTCTGGATTACATGCCAGG	300
Db	1741	TAGAGTTCCCTCTTCACTGCAG	1772		241	CTACACAACTGCTTCACTGAGCTTCACTGCATGTTCTGGATTACATGCCAGG	300
RESULT 3					301	CAGCAGCTGAACACTTGGAGAACATCGATAATCCATTGTCAGGGAGAACATG	360
AAF24791	ID	AAF24791 standard; DNA:	2668 BP.		301	CAGCAGCTGAACACTTGGAGAACATCGATAATCCATTGTCAGGGAGAACATG	360
XX	XX				361	GAGAAAAACCGGGCTGGAGACGAAAGGGAGCAGGTACCGTAGTTCTGAAAGCTGA	420
XX	XX				361	GAGAAAAACCGGGCTGGAGACGAAAGGGAGCAGGTACCGTAGTTCTGAAAGCTGA	420
DT	20-APR-2001	(first entry)			421	ACCCATCTGCGAAATCGCAGATTGGTTCAATTCCAACTTGGACTCTTCAGATTTG	480
DE		Complete nucleotide sequence of a sucrose synthase 3 (Rsus3) promoter.			421	ACCCATCTGCGAAATCGCAGATTGGTTCAATTCCAACTTGGACTCTTCAGATTTG	480
XX	Rice; sucrose synthase 3 promoter; Rsus3 promoter; endosperm expression; transgenic plant; carbohydrate metabolism; sucrose metabolism; ss.				481	GTTCGATGTTGACCGTAGCATCTGAAAATGAAATGGTGTAAATACCTTGAGAGACCT	540
XX	OS	Oryza sativa.			481	GTTCGATGTTGACCGTAGCATCTGAAAATGAAATGGTGTAAATACCTTGAGAGACCT	540
PN	WO200078975-A2.				481	GTTCGATGTTGACCGTAGCATCTGAAAATGAAATGGTGTAAATACCTTGAGAGACCT	540
PD	28-DEC-2000.				541	TCATGAAAGCATGCTGCGCGATAGCTAGAAGAAAATTAATGACTTTGCAA	600
XX	PP	15-JUN-2000;	2000WO-GB002641.		541	TCATGAAAGCATGCTGCGCGATAGCTAGAAGAAAATTAATGACTTTGCAA	600
XX	PR	17-JUN-1999;	99GB-00014210.		601	ACTTAATTGTTGGAGTTGAGTTTGGAGTTGAGTTTGGTGTACTATTGCA	660
XX	PA	(DANI-) DANISCO AS.			601	ACTTAATTGTTGGAGTTGAGTTTGGTGTACTATTGCA	660
XX	PI	Donaldson IA,	Rasmussen TB;		661	GTTTAAACCGCTAATAAGTCAGATAAAATTCTATAGTCATTATAATCATTTT	720
XX	DR	WPI: 2001-071398/08.			661	GTTTAAACCGCTAATAAGTCAGATAAAATTCTATAGTCATTATAATCATTTT	720
XX	PT	Rice sucrose synthase 3 promoter obtainable from plant genus Oryza, useful for expressing nucleotide sequence of interest in specific tissue or cell type e.g. endosperm.			721	TAGTTGGTTGGTCTCATTTCTAACACTTATCAACCATAGCTCACTGATCAATTGCAA	780
PT	PT				721	TAGTTGGTTGGTCTCATTTCTAACACTTATCAACCATAGCTCACTGATCAATTGCAA	780
XX	PS	Disclosure; Fig 3; 144pp; English.			781	AAAAGTTTACTAAACGACATCCCTCATCACACCCAACGCTCACCCATGGTCTCTC	840
XX	CC	The present sequence represents a rice sucrose synthase 3 (Rsus3) promoter. The Rsus3 promoter has low homology with the Rsu1 and Rsu2 promoters (7.8% and 4.6%, respectively). In addition, apart from conserved TATA box and intron splice sites, they have no motifs in common. The promoter can be used to prepare a product of interest, especially in the endosperm of a transgenic plant. Preferably, the promoter is used to cause expression of a nucleotide of interest that can affect carbohydrate metabolism, such as sucrose metabolism, in a plant tissue			781	AAAAGTTTACTAAACGACATCCCTCATCACACCCAACGCTCACCCATGGTCTCTC	840
CC	CC	Sequence 2668 BT; 747 A; 519 C; 572 G; 830 T; 0 U; 0 Other;			841	GACCACGAGTTAGCAGCTTGTGCAACATATGCGTGTGATGAACTCTACTGATGCC	900
CC	CC	The present sequence represents a rice sucrose synthase 3 (Rsus3) promoter. The Rsus3 promoter has low homology with the Rsu1 and Rsu2 promoters (7.8% and 4.6%, respectively). In addition, apart from conserved TATA box and intron splice sites, they have no motifs in common. The promoter can be used to prepare a product of interest, especially in the endosperm of a transgenic plant. Preferably, the promoter is used to cause expression of a nucleotide of interest that can affect carbohydrate metabolism, such as sucrose metabolism, in a plant tissue			841	GACCACGAGTTAGCAGCTTGTGCAACATATGCGTGTGATGAACTCTACTGATGCC	900
CC	CC	Sequence 2668 BT; 747 A; 519 C; 572 G; 830 T; 0 U; 0 Other;			901	ATGGCAATTAGCGTCTGTTCACTGAGCTTCACAAGGCTCAAGGCTGAGGAGCAT	960
CC	CC	Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0;			901	ATGGCAATTAGCGTCTGTTCACTGAGCTTCACAAGGCTCAAGGCTGAGGAGCAT	960
CC	CC	Matches 1772; Conservative			1081	TGTATGGTTAGCCAGCTAACTAATCTCATGGCAAGGGAGCTGCTGATGTTGTGAT	1140
CC	CC	Score 1772; DB 4; Length 2668;			1081	TGTATGGTTAGCCAGCTAACTAATCTCATGGCAAGGGAGCTGCTGATGTTGTGAT	1140
Db	Db	1 ACITTTAGTAATAAGTAAAGTCAACAGAAATAATACTTAAATTCATAATTTATA	60		1081	TGTATGGTTAGCCAGCTAACTAATCTCATGGCAAGGGAGCTGCTGATGTTGTGAT	1140
Db	Db	1 ACITTTAGTAATAAGTAAAGTCAACAGAAATAATACTTAAATTCATAATTTATA	60		1141	GCACCTTCCTCCAGTAATCTAGTGTAAATTTCACAAGGTTGCTCATATGAGCAT	1200
QY	QY	61 AGACGAGTGGTCAAACACTACAAGTAAACACTAAATCCCTTATAATGGGACTTTA	120		1141	GCACCTTCCTCCAGTAATCTAGTGTAAATTTCACAAGGTTGCTCATATGAGCAT	1200
Db	Db	61 AGACGAGTGGTCAAACACTACAAGTAAACACTAAATCCCTTATAATGGGACTTTA	120		1201	AATTGTAATAATTACCAAGGTTCAATTCGGTACCTGACCAATACTACGATGAA	1260
QY	QY	121 TTATGGGACGGGAAAGTGGAGAACATGGCCAGAAAACAAACACCGC	180		1201	AATTGTAATAATTACCAAGGTTCAATTCGGTACCTGACCAATACTACGATGAA	1260
Db	Db	121 TTATGGGACGGGAAAGTGGAGAACATGGCCAGAAAACAAACACCGC	180		1261	GTATCTCGGTTCTGTTGTTGAAACAGCAGAAATAAGCAGAAATTGTGCAA	1320
QY	QY	181 CACCTGGCAGGCATCTTCACTGAGGGTCACTGGTCCGAGAACATGGGACTTAC	240		1261	GTATCTCGGTTCTGTTGTTGAAACAGCAGAAATAAGCAGAAATTGTGCAA	1320
Db	Db	181 CACCTGGCAGGCATCTTCACTGAGGGTCACTGGTCCGAGAACATGGGACTTAC	240		1321	AATTTAATTTAGTTAGTTTTTTAACTTAGCCGGAAAACCTTGAAGTTGTGTCG	1380

Sequence 1686 BP; 527 A; 339 C; 358 G; 462 T; 0 U; 0 Other;							
b	1321	AATTAAATTTAGTTTAACTAGCCGGAAACCTTGAACTTGTGTCGTCG	1380	CC promoter is used to cause expression of a nucleotide of interest that can affect carbohydrate metabolism, such as sucrose metabolism, in a plant tissue			
b	1381	AGCTGCTCGGAAGAACGGTTGGTGGAACTGGTACTGCACITCAT	1440	CC			
b	1381	AGCTGCTCGGAAGAACGGTTGGTGGAACTGGTACTGCACITCAT	1440	CC			
b	1441	TTGAAAGATAATTGCAACGACAATGCCAACGCCATTACCGCAA	1500	XX			
b	1441	TTGAAAGATAATTGCAACGACAATGCCAACGCCATTACCGCAA	1500	SQ	Sequence 1686 BP; 527 A; 339 C; 358 G; 462 T; 0 U; 0 Other;		
b	1501	GCTGAAAGCTTACGATCCCCATACGCCCTGGTCAAACTGCCAAGANGCNGCA	1560	Query Match	95.1%	Score 1686;	DB 4;
b	1501	GCTGAAAGCTTACGATCCCCATACGCCCTGGTCAAACTGCCAAGANGCNGCA	1560	Best Local Similarity	100.0%	Pred. No. 0;	Length 1686;
b	1561	GAAACGGTGTCAATTGTTGCTGGAAAGCCAGTAAGTAAAGAGATGAAATAGT	1620	Matches 1686;	Conservative 0;	Mismatches 0;	
b	1561	GAAACGGTGTCAATTGTTGCTGGAAAGCCAGTAAGTAAAGAGATGAAATAGT	1620	Qy	1 ACTTGTAGATAAAGTAAGTCAGTAAGTAAACTCAAAATTAATTCCAAATTTTTATAA	60	
b	1621	GAGGAACGGGAGTGGATGAGGAGTAGAGATTGAGATGGCAAGAACTTCTGTA	1680	Db	1 ACTTGTAGATAAAGTAAGTCAGTAAGTAAACTCAAAATTAATTCCAAATTTTTATAA	60	
b	1621	GAGGAACGGGAGTGGATGAGGAGTAGAGATTGAGATGGCAAGAACTTCTGTA	1680	Qy	61 AGACGGTGTGTCAAAGTAGCAAGTAAACTCAAAATTAATTCCAAATTTTTATAA	60	
b	1681	TAAATACAGGTGGATGCACTGCTCTCCCACATCCATCGCTCTGCTGTGCA	1740	Db	61 AGACGGTGTGTCAAAGTAGCAAGTAAACTCAAAATTAATTCCAAATTTTTATAA	60	
b	1681	TAAATACAGGTGGATGCACTGCTCTCCCACATCCATCGCTCTGCTGTGCA	1740	Qy	121 TTATGGACGGAGGATCTAGGTGGCAATTGAGATGGTAAAGGATCTACC	180	
b	1741	TAGAGTTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1772	Db	121 TTATGGACGGAGGATCTAGGTGGCAATTGAGATGGTAAAGGATCTACC	180	
b	1741	TAGAGTTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1772	Qy	181 CACCTGGCAGGCATGCACTCTAGGTGGCAATTGAGATGGTAAAGGATCTACC	240	
b	1741	TAGAGTTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1772	Db	181 CACCTGGCAGGCATGCACTCTAGGTGGCAATTGAGATGGTAAAGGATCTACC	240	
b	20-APR-2001	(first entry)		Qy	181 CACCTGGCAGGCATGCACTCTAGGTGGCAATTGAGATGGTAAAGGATCTACC	240	
b	20-APR-2001	(first entry)		Db	181 CACCTGGCAGGCATGCACTCTAGGTGGCAATTGAGATGGTAAAGGATCTACC	240	
b	4			Qy	301 CACCTGGCAGGCATGCACTCTAGGTGGCAATTGAGATGGTAAAGGATCTACC	360	
b	4			Db	301 CACCTGGCAGGCATGCACTCTAGGTGGCAATTGAGATGGTAAAGGATCTACC	360	
b	4			Qy	361 GAGAAAACGGGGCTGGACGAGGAGCACCTGACCGTACGCTGCTGCTGCA	420	
b	4			Db	361 GAGAAAACGGGGCTGGACGAGGAGCACCTGACCGTACGCTGCTGCTGCA	420	
b	421	ACCCATCTGGAAATCCGCAATTGCTGCACTTCGCTTCAAGATTG	480	Qy	421 ACCCATCTGGAAATCCGCAATTGCTGCACTTCGCTTCAAGATTG	480	
b	421	ACCCATCTGGAAATCCGCAATTGCTGCACTTCGCTTCAAGATTG	480	Db	421 ACCCATCTGGAAATCCGCAATTGCTGCACTTCGCTTCAAGATTG	480	
b	481	GTTGGCATGTTCAACCGTACTACATCTGAAAAAATGAGGTAAATACCTTGAGAAGACCT	540	Qy	481 GTTGGCATGTTCAACCGTACTACATCTGAAAAAATGAGGTAAATACCTTGAGAAGACCT	540	
b	481	GTTGGCATGTTCAACCGTACTACATCTGAAAAAATGAGGTAAATACCTTGAGAAGACCT	540	Db	481 GTTGGCATGTTCAACCGTACTACATCTGAAAAAATGAGGTAAATACCTTGAGAAGACCT	540	
b	541	TCATCGAAACATGCTGCGGGCATTTGATTGAGTAATGAAAGAAATTAATGCTACTTTGCAA	600	Qy	541 TCATCGAAACATGCTGCGGGCATTTGATTGAGTAATGAAAGAAATTAATGCTACTTTGCAA	600	
b	541	TCATCGAAACATGCTGCGGGCATTTGATTGAGTAATGAAAGAAATTAATGCTACTTTGCAA	600	Db	541 TCATCGAAACATGCTGCGGGCATTTGATTGAGTAATGAAAGAAATTAATGCTACTTTGCAA	600	
b	601	ACTTAATTGGATGTTAGTTTCCATGTTAGTGTATTCTACTATGCA	660	Qy	601 ACTTAATTGGATGTTAGTTTCCATGTTAGTGTATTCTACTATGCA	660	
b	601	ACTTAATTGGATGTTAGTTTCCATGTTAGTGTATTCTACTATGCA	660	Db	601 ACTTAATTGGATGTTAGTTTCCATGTTAGTGTATTCTACTATGCA	660	
b	661	GTAAACCGCTTAATAGTCAGATAAAATTCTATAGATCATTTAAATCTATT	720	Qy	661 GTAAACCGCTTAATAGTCAGATAAAATTCTATAGATCATTTAAATCTATT	720	
b	661	GTAAACCGCTTAATAGTCAGATAAAATTCTATAGATCATTTAAATCTATT	720	Db	661 GTAAACCGCTTAATAGTCAGATAAAATTCTATAGATCATTTAAATCTATT	720	
b	721	TAGTTGCTTCTGTTCACTTCTACCACTTCAACATGCTAACTGACAA	780	Qy	721 TAGTTGCTTCTGTTCACTTCTACCACTTCAACATGCTAACTGACAA	780	
b	721	TAGTTGCTTCTGTTCACTTCTACCACTTCAACATGCTAACTGACAA	780	Db	721 TAGTTGCTTCTGTTCACTTCTACCACTTCAACATGCTAACTGACAA	780	
b	781	TAAAGTACTAACGAGATCGTCATCAACCCAAACGTCACTGCTTC	840	Qy	781 TAAAGTACTAACGAGATCGTCATCAACCCAAACGTCACTGCTTC	840	
b	781	TAAAGTACTAACGAGATCGTCATCAACCCAAACGTCACTGCTTC	840	Db	781 TAAAGTACTAACGAGATCGTCATCAACCCAAACGTCACTGCTTC	840	
b	841	GACCAAGAGTTAGCACTTGTGCTGAACTATATGGTGGATGACATCTACTGTCGCGC	900	Qy	841 GACCAAGAGTTAGCACTTGTGCTGAACTATATGGTGGATGACATCTACTGTCGCGC	900	
b	841	GACCAAGAGTTAGCACTTGTGCTGAACTATATGGTGGATGACATCTACTGTCGCGC	900	Db	841 GACCAAGAGTTAGCACTTGTGCTGAACTATATGGTGGATGACATCTACTGTCGCGC	900	
b	901	ATGGGAATTTCGGTTGTTCAACCTTCAACGGCACAGCTGAGACAT	960	Qy	901 ATGGGAATTTCGGTTGTTCAACCTTCAACGGCACAGCTGAGACAT	960	
b	901	ATGGGAATTTCGGTTGTTCAACCTTCAACGGCACAGCTGAGACAT	960	Db	901 ATGGGAATTTCGGTTGTTCAACCTTCAACGGCACAGCTGAGACAT	960	

Db	541	ATATACCAAGGTTCATACTCCGTTACTGACCAAAATACACTCACGANTGGPATCCT	600	XX
Qy	1269	GGTTTCTGTTAACACCGTGTAAACCGGAAATAAGGAAATTGCAAATTAA	1328	CC
Db	601	GGTTTCTGTTAACACCGTGTAAACCGGAAATAAGGAAATTGCAAATTAA	660	CC
Qy	1329	ATTTAG-TTTCCTTTTAACTTAGCCGGAAACCTTGAGTTGTGTGCTGAGCTG	1386	CC
Db	661	ATTTAGTGTTCCTTTTAACTTAGCCGGAAACCTTGAGTTGTGTGCTGAGCTG	720	CC
Qy	1387	CCTGGAAAGGACGGTTGGTGGATTGTGAACCTGGTACTGCACTCATTTGAA	1446	CC
Db	721	CCTGGAAAGGACGGTTGGTGGATTGTGAACCTGGTACTGCACTCATTTGAA	780	XX
Qy	1447	CAGATATTAGTGCACAGACAATGCCAAGCATTTCCTGTTACCGGCAGCTGA	1506	Query Match 4.9%; Score 86; DB 4; Length 86;
Db	781	CAGATATTAGTGCACAGACAATGCCAAGCATTTCCTGTTACCGGCAGCTGA	840	Best Local Similarity 100.0%; Pred. No. 5e-30; Mismatches 0; Indels 0; Gaps 0;
Qy	1507	GCTTTACGTTCCCTCCATACGCCGTTGCTGCAACCTGCAAGAAAGCAGGAAACA	1566	Qy 1687 CAGGTGATGATGGCTCCAGATCCATGGTTCTGGTTCTGGTCTGAGT 1746
Db	841	GCTTTACGTTCCCTCCATACGCCGTTGCTGCAACCTGCAAGAAAGCAGGAAACA	900	Db 1 CAGGTGATGATGGCTCCAGATCCATGGTTCTGGTCTGAGT 60
Qy	1567	GGTGCATTTGTGTGGTAAAGGCAAGTAAGTAAACAGAGATGGAAATGTGAGGAC	1626	Qy 1747 TTCCCTCTCTCTCTCTCTAGTCAGTGCAAG 1772
Db	901	GGTGCATTTGTGTGGTAAAGGCAAGTAAGTAAACAGAGATGGAAATGTGAGGAC	960	Db 61 TTCCCTCTCTCTCTCTAGTCAGTGCAAG 86
Qy	1627	CAGGGAGTGGCAGGGGAACATGGCCCAAGCCTCCCTGCACTTTGTTGATAAATA	1686	RESULT 7 ADA72764/c
Db	961	CAGGGAGTGGCAGGGGAACATGGCCCAAGCCTCCCTGCACTTTGTTGATAAATA	1020	ID ADA72764 standard; DNA; 2000 BP.
Qy	1687	CAGGTGGATGATGGCTCCAGATCCATCGGTTCTCTGCTCTGTTATCCATAGACT	1746	XX
Db	1021	CAGGTGGATGATGGCTCCAGATCCATCGGTTCTCTGCTCTGTTATCCATAGACT	1080	AC ADA72764;
Qy	1747	TTCCTCCCTCTCTCTCCTT 1763	DT 20-NOV-2003 (first entry)	
Db	1081	TTCCTCCCTCTCCTT 1097	XX	
RESULT 6 AAF24788		Rice; sucrose synthase 3 promoter; endosperm expression; transgenic plant; carbohydrate metabolism; sucrose metabolism; ss. Oryza sativa.	DB Rice gene, SEQ ID 6089.	
XX		XX	XX	
AC AAF24788;		OS Oryza sativa.	OS	
XX		XX	XX	
DT 20-APR-2001 (first entry)		PN WO201000898-A1.	PN	
XX		XX	XX	
DE Nucleotide sequence of a sucrose synthase 3 (RSus3) promoter fragment.		PD 03-JAN-2003.	PD	
XX		XX	XX	
KW rice; sucrose synthase 3 promoter; RSus3 promoter; endosperm expression; transgenic plant; carbohydrate metabolism; sucrose metabolism; ss.		PF 22-JUN-2001; 2001WO-1B001105.	PF	
XX		XX	XX	
PR 17-JUN-1999; 99GB-00014210.		PR 22-JUN-2001; 2001WO-1B001105.	PR	
XX		XX	XX	
PA (DANI-) DANISCO AS.		(SIGN) SYNGENTA PARTICIPATIONS AG.	PA	
XX		PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y, Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;	PI	
DR WPI; 2003-175290/17.		XX	PI XX	
XX		XX	DR	
PT Identifying at least one gene involved in plant resistance or response to pathogenic infection for conferring resistance or tolerance to a plant to bacterial, fungal or viral infection by determining or detecting plant gene expression.		XX	XX	
PR 15-JUN-2000; 2000WO-GB002641.		PT 28-DEC-2000.	PT	
XX		XX	PT	
PR 17-JUN-1999; 99GB-00014210.		XX	PT	
XX		XX	PT	
PA Donaldson IA, Rasmussen TB; DR WPI; 2001-071398/08.		XX	PT	
XX		XX	PT	
PT Rice sucrose synthase 3 promoter obtainable from plant genus Oryza, useful for expressing nucleotide sequence of interest in specific tissue or cell type e.g. endosperm.		XX	PT	
PS Disclosure; Page 143; 144pp; English.		XX	PS	

XX Sequence 2000 BP; 623 A; 475 C; 360 G; 539 T; 0 U; 3 Other;
 Query Match 2.5%; Score 45; DB 7; Length 2000;
 Best Local Similarity 100.0%; Pred. No. 1.1e-10;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 CAAATTTTAATAGACGAGTGGTCAAACAGTACAAGTAAAAA 90
 Db 294 CAAATTTTAATAGACGAGTGGTCAAACAGTACAAGTAAAAA 250

RESULT 8
 ADA72806 standard; DNA; 2000 BP.
 ID ADA72806 standard; DNA; 2000 BP.
 XX
 AC ADA72806;
 XX DT 20-NOV-2003 (first entry)
 XX DE Rice gene, SEQ ID 6131.
 XX PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX PA Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
 XX PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
 XX PR 2003-175290/17.
 XX WO200300898-A1.
 XX PN WO200300898-A1.
 XX PD 03-JAN-2003.
 XX PR 22-JUN-2001; 2001WO-IB001105.
 XX PR 22-JUN-2001; 2001WO-IB001105.
 XX PR 22-JUN-2001; 2001WO-IB001105.
 XX PR 22-JUN-2001; 2001WO-IB001105.

XX PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX PA Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
 XX PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
 XX DR 2003-175290/17.
 XX PT Identifying at least one gene involved in plant resistance or response to pathogenic infection for conferring resistance or tolerance to a plant to bacterial, fungal or viral infection by determining or detecting plant gene expression.
 XX PS Claim 27; SEQ ID NO 5846; 899pp; English.
 XX PA The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.
 XX SQ Sequence 2000 BP; 649 A; 378 C; 372 G; 601 T; 0 U; 0 Other;
 XX PS Claim 27; SEQ ID NO 6131; 899pp; English.
 XX PA The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.
 XX SQ Sequence 2000 BP; 575 A; 481 C; 470 G; 467 T; 0 U; 7 Other;
 XX PS Sequence 2000 BP; 575 A; 481 C; 470 G; 467 T; 0 U; 7 Other;
 XX Query Match 1.9%; Score 34; DB 7; Length 2000;
 XX Best Local Similarity 100.0%; Pred. No. 1.7e-05;
 XX Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 TTTTTATAAGACGAGTGGTCAAACAGTACAG 84
 Db 661 TTTTTATAAGACGAGTGGTCAAACAGTACAG 694

RESULT 9
 ADA72521

ID ADA72521 standard; DNA; 2000 BP.
 XX
 AC ADA72521;
 XX DT 20-NOV-2003 (first entry)
 XX DE Rice gene, SEQ ID 5846.
 XX KW Plant; bacterial infection; fungal infection; viral infection; rice;
 XX Gene; ds.
 XX OS Oryza sativa.
 XX PN WO200300898-A1.

Query Match 1.8%; Score 32; DB 7; Length 2000;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 AAAATAATAATAATTCCAAATTTTTTAATA 60
 Db 516 AAAATAATAATAATTCCAAATTTTTTAATA 547

RESULT 10
 ADA73205/c
 ID ADA73205 standard; DNA; 2000 BP.
 XX
 AC ADA73205;
 XX DT 20-NOV-2003 (first entry)
 XX DE Rice gene, SEQ ID 6531.
 XX KW Plant; bacterial infection; fungal infection; viral infection; rice;
 XX Gene; ds.
 XX OS Oryza sativa.
 XX PN WO200300898-A1.

XX 03-JAN-2003 .
 PD 22-JUN-2001; 2001WO-IB001105.
 PF XX
 PR XX
 22-JUN-2001; 2001WO-IB001105.
 XX
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y; Karagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G; DR WPI; 2003-175290/17.
 PT Identifying at least one gene involved in plant resistance or response to pathogenic infection for conferring resistance or tolerance to a plant to bacterial, fungal or viral infection by determining or detecting plant gene expression.
 XX
 PA Claim 27; SEQ ID NO 6668; 899pp; English.
 XX
 The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.
 XX
 PS SQ Sequence 2000 BP; 638 A; 344 C; 433 G; 583 T; 0 U; 2 Other;
 XX
 Query Match 1.6†; Score 28; DB 7; Length 2000;
 Best Local Similarity 100.0%; Pred. No. 0.011; Mismatches 0; Indels 0; Gaps 0;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 29 AAATATAATATAATTCCAAATTTTTT 56
 Db 292 AAATATAATATAATTCCAAATTTTTT 319
 XX
 RESULT 12
 ID AAL46958/C
 XX
 Query Match 1.6†; Score 28; DB 7; Length 2000;
 Best Local Similarity 100.0%; Pred. No. 0.0013; Mismatches 0; Indels 0; Gaps 0;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 47 AAATTTTTATAAAGACCGTGTCAAC 76
 Db 367 AAATTTTTATAAAGACGAGGTGTCAAC 338
 XX
 RESULT 11
 ID ADA73342
 XX
 AC ADA73342 ;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Rice gene, SEQ ID 6668.
 XX
 KW Plant; bacterial infection; fungal infection; viral infection; rice; gene; ds.
 XX
 OS Oryza sativa.
 XX
 PN WO2003000898-A1.
 XX
 PD 03-JAN-2003.
 XX
 PR 22-JUN-2001; 2001WO-IB001105.
 XX
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y; Karagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G; DR WPI; 2003-175290/17.
 XX
 DR P-PSDB; AAQ17798.
 XX

PT Identifying at least one gene involved in plant resistance or response to pathogenic infection for conferring resistance or tolerance to a plant to bacterial, fungal or viral infection by determining or detecting plant gene expression.
 XX
 PS XX
 The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.
 XX
 SQ Sequence 2000 BP; 638 A; 344 C; 433 G; 583 T; 0 U; 2 Other;
 XX
 Query Match 1.6†; Score 28; DB 7; Length 2000;
 Best Local Similarity 100.0%; Pred. No. 0.011; Mismatches 0; Indels 0; Gaps 0;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 29 AAATATAATATAATTCCAAATTTTTT 56
 Db 292 AAATATAATATAATTCCAAATTTTTT 319
 XX
 RESULT 12
 ID AAL46958/C
 XX
 Key AC AAL46958; standard; cDNA; 5579 BP.
 exon AC
 XX
 FT 3177. .3947
 FT /*tag= b
 FT /number= 1
 FT 30-AUG-2002 (first entry)
 FT 3711. .5327
 FT Rice lesion inhibitor protein Sp17 coding sequence.
 DE XX
 KW XX
 DE Rice; lesion formation inhibition; heat stress; agriculture; Sp17;
 KW XX
 DE transgenic; plant; horticulture; gene; ss.
 KW XX
 OS Oryza sativa.
 OS XX
 FH Key
 exon FT Location/Qualifiers
 XX FT 3177. .3947
 FT FT /*tag= b
 FT FT /number= 1
 FT CDS FT 3711. .5327
 FT FT /*tag= a
 FT FT /product= "Sp17"
 FT intron FT 3948. .4184
 FT FT /*tag= c
 FT FT /number= 1
 FT exon FT 4185. .5327
 FT FT /*tag= d
 FT FT /number= 2
 XX PN WO2003033092-A1.
 XX
 PD 25-APR-2002.
 XX
 PR 18-OCT-2001; 2001WO-JP0009153.
 XX
 PR 18-OCT-2000; 2000JP-00318857.
 XX
 PA (NAG-) NAT INST AGROBIOLOGICAL SCI.
 XX
 PI Yano M, Yamamoto U;
 XX
 DR WPI; 2002-372312/40.
 DR P-PSDB; AAQ17798.
 XX

PT Rice-originated gene, Sp17, that inhibits lesion formation and is applicable in improving heat stress of plants thus leading to prevention of lesion formation, for developing new breeds of plants for agriculture and horticulture.

XX Claim 1; Page 30-40; 53pp; Japanese.

XX The present invention provides the protein and coding sequences of rice lesion formation inhibitor Sp17. The protein improves the heat stress of the plant, and can be used in the development of new breeds of plants for agriculture and horticulture. The present sequence is the coding sequence of the invention.

Sequence 5579 BP; 1453 A; 1272 C; 1235 G; 1619 T; 0 U; 0 Other;

Query Match Score 1.6%; Score 28; DB 6; Length 5579;

Best Local Similarity 100.0%; Pred. No. 0.011; Mismatches 0;

Matches 28; Conservative 0; Indels 0; Gaps 0;

Qy 57 AATAAGCAGGAGGGTCAAACTACAG 84

Db 2210 AATAAGCAGGAGGGTCAAACTACAG 2183

RESULT 13

ADA73166/C

ID ADA73166 standard; DNA; 2000 BP.

XX AC ADA73166;

XX DT 20-NOV-2003 (first entry)

XX DE Rice gene, SEQ ID 6492.

XX PA Plant; bacterial infection; fungal infection; viral infection; rice;

XX KW gene; ds.

XX OS Oryza sativa.

XX PN WO200300898-A1.

XX PD 03-JAN-2003.

XX XX 22-JUN-2001; 2001WO-IB001105.

XX PR 22-JUN-2001; 2001WO-IB001105.

XX XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX PA Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;

XX PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;

XX DR WPI; 2003-175290/17.

XX XX Identifying at least one gene involved in plant resistance or response to pathogenic infection for conferring resistance or tolerance to a plant to bacterial, fungal or viral infection by determining or detecting plant gene expression.

XX PS Claim 27; SEQ ID NO 6524; 899pp; English.

XX PA (SYGN) SYNGENTA PARTICIPATIONS AG.

XX PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;

XX PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;

XX DR WPI; 2003-175290/17.

XX XX Identifying at least one gene involved in plant resistance or response to pathogenic infection for conferring resistance or tolerance to a plant to bacterial, fungal or viral infection by determining or detecting plant gene expression.

XX PS Sequence 2000 BP; 633 A; 407 C; 355 G; 604 T; 0 U; 1 Other;

XX XX PA Score 1.5%; Score 26; DB 7; Length 2000;

CC Best Local Similarity 100.0%; Pred. No. 0.1;

CC Matches 26; Conservative 0; Mismatches 0;

CC Indels 0; Gaps 0;

CC Qy 1 ACTTAGATAATAAGTAAGTCACAA 26

CC ||||| ||||| ||||| ||||| ||||| ||||| |||||

CC Db 108 ACTTAGATAATAAGTAAGTCACAA 133

CC ||||| ||||| ||||| ||||| ||||| ||||| |||||

CC RESULT 15

CC AAF81474/C

CC ID AAP81474 standard; DNA; 676 BP.

XX SQ Sequence 2000 BP; 492 A; 534 C; 468 G; 504 T; 0 U; 2 Other;

XX SQ

AC AAF81474;
 XX DT 08-JUN-2001 (first entry)
 XX DE Corn promoter clone #700345819.
 XX KW Corn; promoter; transgenic plant; herbicide resistance; ds.
 XX OS Zea mays.
 XX PN WO200119976-A2.
 XX PD 22-MAR-2001.
 XX PF 13-SEP-2000; 2000WO-US025078.
 XX PR 16-SEP-1999; 99US-0154182P.
 XX PA (MONS) MONSANTO CO.
 PI Anderson HM, Chay CA, Chen G, Conner TW;
 XX DR WPI; 2001-244796/25.
 XX PT Novel promoter nucleic acid sequences useful for regulating heterologous
 PT gene expression in plants, comprising regulatory sequences located
 PT upstream to plant DNA structural coding sequences.
 PS Claim 1; Page 98; 101pp; English.

XX The present invention relates to novel corn promoter sequences (see
 CC AAF81456-AAF81478). The promoter sequences are useful for conferring
 CC expression of a second polynucleotide molecule in a transgenic plant
 CC tissue. In addition, the promoter sequences are useful for providing
 CC plants with herbicide resistance. The promoter sequences are suitable for
 CC selectively modulating expression of any operatively linked gene and
 CC provide additional regulatory element diversity in a plant expression
 CC vector in gene stacking approaches. The present sequence is one such corn
 CC promoter sequence isolated in the present invention
 XX Sequence 676 BP; 210 A; 152 C; 119 G; 195 T; 0 U; 0 Other;
 SQ

Query Match 1.4%; Score 24; DB 4; Length 676;
 Best Local Similarity 100.0%; Pred. No. 0.91;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 51 TTTTTATAAGCGAGTGGTCA 74
 Db 226 TTTTTATAAGCGAGTGGTCA 203

Search completed: October 2, 2004, 10:13:35
 Job time : 1029 secs



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OM nucleic - nucleic search, using sw model

Run on: October 2, 2004, 08:40:19 ; Search time 153 Seconds
(without alignments)
6427.274 Million cell updates/sec

Title: US-10-009-570-1
Perfect score: 1772
Sequence: 1 acttttagataaaatgttaag.....ctcttctcccttcagtgcagg 1772

Scoring table: OLIGO_NUC
Gapext: 60.0
Gapop: 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	24	1.4	6776	4	US-09-665-189A-71
C 2	23	1.3	90541	4	US-09-759-359A-3
C 3	23	1.3	193303	4	US-09-497-855A-37
C 4	23	1.3	193303	4	US-09-497-855A-44
C 5	20	1.1	177	4	US-09-313-294A-292
C 6	20	1.1	888	4	US-09-134-001C-13
C 7	20	1.1	1462	2	US-08-246-316A-30
C 8	20	1.1	1462	3	US-08-453-772-30
C 9	20	1.1	1462	5	PCT-US93-050-30
C 10	20	1.1	1462	5	PCT-US93-050-30
C 11	19	1.1	531	3	US-08-642-274D-39
C 12	19	1.1	531	3	US-08-952-014C-39
C 13	19	1.1	573	4	US-09-124-001A-301
C 14	19	1.1	851	4	US-09-495-050A-138
C 15	19	1.1	2095	4	US-09-227-357-31
C 16	19	1.1	6113	4	US-10-204-708-14
C 17	19	1.1	6574	4	US-09-221-017B-1097
C 18	19	1.1	6669	4	US-10-204-708-6
C 19	19	1.1	6678	3	US-08-816-617A-1
C 20	19	1.1	11049	4	US-10-204-708-23
C 21	19	1.1	25464	4	US-09-326-480A-4
C 22	19	1.1	70000	4	US-09-851-96-3
C 23	19	1.1	392000	4	US-10-027-983-11
C 24	19	1.1	1830121	4	US-09-257-884-1
C 25	19	1.1	1830121	4	US-09-643-990A-1
C 26	18	1.0	405	4	US-09-621-976-15602
C 27	18	1.0	562	5	PCT-US92-03993-6

%
ALIGMENTS

RESULT 1
US-09-665-189A-71/C
; Sequence 71, Application US/09665189A
; Patent No. 6645765
; GENERAL INFORMATION:
; APPLICANT: Anderson, Heather
; APPLICANT: Chay, Catherine
; APPLICANT: Conner, Guilan
; APPLICANT: Connex, Timothy
; TITLE OF INVENTION: Plant Regulatory Sequences for Control of Gene Expression
; FILE REFERENCE: 38-211 (15674) B
; CURRENT APPLICATION NUMBER: US/09/665-189A
; CURRENT FILING DATE: 2000-09-15
; PRIORITY NUMBER: 09/665,189
; PRIORITY FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 75
; SEQ ID NO: 71
; SOFTWARE: PatentIn version 3.0
; TYPE: DNA
; ORGANISM: Zea mays
; US-09-665-189A-71

Query Match 1.4% ; Score 24; DB 4; Length 676;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 TTTTTATAAGACGACTGGCTCAA 74
Db 226 TTTTTATAAGACGACTGGCTCAA 203

RESULT 2
US-09-759-359A-3/C
; Sequence 3, Application US/09759359A
; Patent No. 6492153
; GENERAL INFORMATION:
; APPLICANT: ABU-TREIDAH, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES THEREOF
; FILE REFERENCE: C1001043
; CURRENT APPLICATION NUMBER: US/09/759,359A
; CURRENT FILING DATE: 2001-01-16
; PRIORITY NUMBER: 09/759,359A
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 3
; LENGTH: 90541
; TYPE: DNA
; ORGANISM: Human

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US-09-759-359A-3

Query Match      1.3%; Score 23; DB 4; Length 90541;
Best Local Similarity    100.0%; Pred. No. 0.33;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          14 AAGTAAGTCACAGAAATAAA 36
Db          17920 AACTAAGTCACAGAAATAAA 17898

RESULT 3
US-09-497-855A-37
Sequence 37, Application US/09497855A
; Patent No. 6605432
GENERAL INFORMATION
; APPLICANT: Huang, Tim
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
; FILE REFERENCE: US091523
; CURRENT APPLICATION NUMBER: US/09/497, 855A
; CURRENT FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/120, 592
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 60/118, 760
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
; LENGTH: 1933303
; TYPE: DNA
; ORGANISM: Homo sapiens;
TIS-09-497-855A-37

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RESULT 4
US -09-497-855A-44
; Sequence 44, Application US/09497855A
; Patent No. 6605432
; GENERAL INFORMATION:
; APPLICANT: Huang, Tim
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
; FILE REFERENCE: UMO11523
; CURRENT APPLICATION NUMBER: US/09/497,855A
; CURRENT FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/120,592
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 60/118,760
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.0

SEQ ID NO	LENGTH:	TYPE:	ORGANISM:	US-09-497-855A-44	Query Match	Score	DB 4;	Length	193303;	Gaps
44	193303	DNA	Homo sapiens;		Best Local Similarity	1.3%;	DB 4;			0;
					Matches	100.0%;	Pred.	No.		Mismatches
					23;	Conservative	0;	0.32;		Indels
										0;
Qy	1744	AGTTCCCTCCCTTCCTCCTCTTCTG	1766							
Dh	166834	AGTTCCCTCCCTTCCTCCTCTTCTG	166856							

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RESULT 5
US-09-313-294A-292/c
; Sequence 292, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Laligudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO: 292
; LENGTH: 177
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 647
; NAME/KEY: unsure
; LOCATION: 2, 6, 75-93
; OTHER INFORMATION: a, t, c, g, or ot
US-09-313-294A-292
Query Match          1.1%; Score
Best Local Similarity 100.0%; Pred.
Matches 20; Conservative 0; Mis
950 AGCAGAGGCAATGCCATGCGATCTG 969

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RESULT 6
US-09-134-001C-13/C
; Sequence 13, Application US/09134001C
; Patent No. 380370
; GENERAL INFORMATION:

RESULT 7
US-08-464-517-30
Sequence 30, Application US/08464517
350 GILDED CAGNAZI U.S.A.

Patent No. 5869640
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,361A
FILING DATE: 19-MAY-1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 1462 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: join(378..569, 662..1000, 1040..1189,
US-08-246-361A-30)

Query Match 1.1% Score 20; DB 2; Length 1462;
Best Local Similarity 100.0%; Pred. No. 9.7; Mismatches 0; Indels 0; Gaps 0;

Qy 158 AAAACAAACAAACACAC 177
Db 310 AAAACAAACAAACAC 329

RESULT 9
US-08-463-772-30
; Sequence 30, Application US/08463772
; GENERAL INFORMATION:
; Patent No. 606501
; APPLICANT: BEACH, David H.
; TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,772
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308

FILING DATE: 16-OCT-1992
 APPLICATION NUMBER: US 07/888,178
 PRIORITY APPLICATION DATA:
 FILING DATE: 26-MAY-1992
 APPLICATION NUMBER: US 07/701,514
 ATTORNEY/AGENT INFORMATION:
 NAME: Matthew P. Vincent
 REGISTRATION NUMBER: 36,709
 REFERENCE/DOCKET NUMBER: MLI-004C
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 227-5941
 INFORMATION FOR SEQ ID NO: 30:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1462 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: join(378..569, 662..1000, 1040..1189,
 i LOCATION: 1191..1292, 1292..1324)
 US-08-463-772-30

Query Match 1.1%; Score 20; DB 3; Length 1462;
 Best Local Similarity 100.0%; Pred. No. 9.7; Indels 0; Gaps 0;

RESULT 10
 PCT-US93-05000-30
 GENERAL INFORMATION:
 APPLICANT: MITOTIX
 TITLE OF INVENTION: D-Type Cyclin and Uses Related Thereto
 NUMBER OF SEQUENCES: 42
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 STREET: Two Millettia Drive
 CITY: Lexington
 STATE: Massachusetts
 COUNTRY: US
 ZIP: 02173
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/05000
 FILING DATE: 1990525
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/888,178
 FILING DATE: 26-MAY-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Granahan, Patricia
 REGISTRATION NUMBER: 32,227
 REFERENCE/DOCKET NUMBER: CSHL91-02A
 TELECOMMUNICATION INFORMATION:
 TELEFAX: 617-861-6240
 INFORMATION FOR SEQ ID NO: 30:
 LENGTH: 1462 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: double

; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; PCT-US93-05000-30
 Query Match 1.1%; Score 20; DB 5; Length 1462;
 Best Local Similarity 100.0%; Pred. No. 9.7; Indels 0; Gaps 0;
 Qy 158 AAAACAAACAAACACAC 177
 Db 310 AAAACAAACAAACACAC 329

RESULT 11
 US-08-642-274D-39
 Sequence 39, Application US/08642274D
 ; Patent No. 6200749
 ; GENERAL INFORMATION:
 ; APPLICANT: Shiloh, Yosef
 ; TITLE OF INVENTION: MUTATED FORMS OF THE ATAXIA-TELANGIECTASIA GENE AND METHOD TO
 ; SCREEN FOR A PARTIAL A-T PHENOTYPE
 ; FILE REFERENCE: 229000033
 ; CURRENT APPLICATION NUMBER: US/08/642,274D
 ; NUMBER OF SEQ ID NOS: 220
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 39
 ; LENGTH: 531
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: genomic

Query Match 1.1%; Score 19; DB 3; Length 531;
 Best Local Similarity 100.0%; Pred. No. 30; Indels 0; Gaps 0;

Qy 1321 AATTAAATTTAGTTT 1339
 Db 105 AATTAAATTTAGTTT 123

RESULT 12
 US-08-952-014C-39
 Sequence 39, Application US/08952014C
 ; Patent No. 6265158
 ; GENERAL INFORMATION:
 ; APPLICANT: Shiloh, Yosef
 ; TITLE OF INVENTION: ATAXIA-TELANGIECTASIA GENE AND ITS GENOMIC ORGANIZATION
 ; NUMBER OF SEQUENCES: 91
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Kohn & Associates
 ; STREET: 30500 No. 6265158Western Hwy., Suite 410
 ; CITY: Farmington Hills
 ; STATE: Michigan
 ; COUNTRY: U.S.
 ; ZIP: 48334
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US93/05000
 ; FILING DATE: 1990525
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/888,178
 ; FILING DATE: 26-MAY-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Granahan, Patricia
 ; REGISTRATION NUMBER: 32,227
 ; REFERENCE/DOCKET NUMBER: CSHL91-02A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEFAX: 617-861-6240
 ; INFORMATION FOR SEQ ID NO: 30:
 ; LENGTH: 1462 base pairs
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: double

TELEPHONE: 810-539-5050
 TELEFAX: 810-539-5055
 INFORMATION FOR SEQ ID NO: 39:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 531 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-952-014C-39

Query Match Score 1.1%; Best Local Similarity 100.0%; Pred. No. 30; Length 531;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1321 AATTAAATTTAGTTT 1339
 Db 105 AATTAAATTTAGTTT 123

RESULT 13
 US-09-134-001C-301/c
 Sequence 301, Application US/09134001C
 Patent No. 6380370
 GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 FILE REFERENCE: GTC-007
 CURRENT APPLICATION NUMBER: US/09/134,001C
 CURRENT FILING DATE: 1998-08-13
 PRIORITY NUMBER: US 60/064,964
 PRIOR FILING DATE: 1997-11-08
 PRIOR APPLICATION NUMBER: US 60/055,779
 PRIOR FILING DATE: 1997-08-14
 NUMBER OF SEQ ID NOS: 5674
 SEQ ID NO 301
 LENGTH: 573
 TYPE: DNA
 ORGANISM: *Staphylococcus epidermidis*
 US-09-134-001C-301

Query Match Score 1.1%; Best Local Similarity 100.0%; Pred. No. 30; Length 573;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 710 TAATCATTTAGTTGTT 728
 Db 99 TAATCATTTAGTTGTT 81

RESULT 14
 US-09-495-050A-138/c
 Sequence 138, Application US/09495050A
 Patent No. 6492505
 GENERAL INFORMATION:
 APPLICANT: Roopa, Reddy
 APPLICANT: Guegler, Karl, J.
 APPLICANT: Au-Young, Janice
 TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED E
 FILE REFERENCE: PA-0013 US
 CURRENT APPLICATION NUMBER: US/09/495,050A
 CURRENT FILING DATE: 2000-01-31
 PRIOR APPLICATION NUMBER: 60/118,318
 PRIOR FILING DATE: February 1, 1999
 NUMBER OF SEQ ID NOS: 305
 SOFTWARE: PERL Program
 SEQ ID NO 138
 LENGTH: 851
 TYPE: DNA
 ORGANISM: *Homo sapiens*
 FEATURE:
 NAME/KEY: misc_feature

EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,684
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,984
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,954
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/058,785
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,664
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,660
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,661
NUMBER OF SEQ ID NOS: 672
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 31
LENGTH: 2095
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (14)
OTHER INFORMATION: n equals a,t,g, or c
US-09-227-357-31

Query Match 1.1%; Score 19; DB 4; Length 2095;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	158 AAAAGAAACAAACACA 176
Db	489 AAAAGAAACAAACACA 471

Search completed: October 2, 2004, 15:15:58
Job time : 157 secs

Result	No.	Score	Match	Length	DB ID	Description
c	1	39	2.2	1610	17	US-10-437-963-4401 Sequence 4401, AP
c	2	37	2.1	2981	17	US-10-437-963-4401 Sequence 59741, A
c	3	28	1.6	5579	13	US-10-437-963-4401 Sequence 91213, A
c	4	27	1.5	2000	16	US-10-437-963-4401 Sequence 36681, A
c	5	26	1.5	630	17	US-10-437-963-4401 Sequence 1256, A
c	6	25	1.4	858	13	US-10-437-963-4401 Sequence 1664, AP
c	7	25	1.4	2000	16	US-10-437-963-4401 Sequence 1, Appli
c	8	25	1.4	6064	17	US-10-437-963-4401 Sequence 258, AP
c	9	25	1.4	367778	15	US-10-437-963-4401 Sequence 240, AP
c	10	24	1.4	359	17	US-10-437-963-4401 Sequence 45, Appli
c	11	24	1.4	390	13	US-10-437-963-4401 Sequence 64432, A
c	12	24	1.4	467	17	US-10-437-963-4401 Sequence 86792, A
c	13	24	1.4	1480	17	US-10-437-963-4401 Sequence 43365, A
c	14	24	1.4	2000	16	US-10-437-963-4401 Sequence 1731, AP

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	DB ID	Description
c	1	39	2.2	1610	17	US-10-437-963-7688 Sequence 7688, AP
c	2	37	2.1	2981	17	US-10-437-963-7688 Sequence 92628, A
c	3	28	1.6	5579	13	US-10-437-963-7688 Sequence 1, Appli
c	4	27	1.5	2000	16	US-10-437-963-7688 Sequence 1731, AP
c	5	26	1.5	630	17	US-10-437-963-7688 Sequence 27816, A
c	6	25	1.4	858	13	US-10-437-963-7688 Sequence 718, AP
c	7	25	1.4	2000	16	US-10-437-963-7688 Sequence 2163, AP
c	8	25	1.4	6064	17	US-10-437-963-7688 Sequence 10006, A
c	9	25	1.4	367778	15	US-10-437-963-7688 Sequence 2, Appli
c	10	24	1.4	359	17	US-10-437-963-7688 Sequence 8728, A
c	11	24	1.4	390	13	US-10-437-963-7688 Sequence 64432, A
c	12	24	1.4	467	17	US-10-437-963-7688 Sequence 86792, A
c	13	24	1.4	1480	17	US-10-437-963-7688 Sequence 43365, A
c	14	24	1.4	2000	16	US-10-437-963-7688 Sequence 1731, AP

RESULT 2

```

US-10-437-963-92628 Application US/10447963
; Sequence 92628, Application US/10447963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; Title of Invention: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 24966
; SEQ ID NO 9628 LENGTH: 2981
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(2981)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_91091C.1
US-10-437-963-92628

Query Match Similarity 2.1%; Score 37; DB 17; Length 2981;
Best Local Similarity 100.0%; Pred. No. 8.5e-08;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1727 GCCTGGTCATCCATAGACTTCTCCCTTCCTCCCTT 1763
Db          152 GCCTGGTCATCCATAGACTTCTCCCTTCCTCCCTT 188

RESULT 3
US-10-168-273B-1/C
; Sequence 1, Application US/10168273B
; Publication No. US20040058324A1
; GENERAL INFORMATION:
; APPLICANT: Yano, Masahiro
; APPLICANT: Yamanouchi, Utako
; TITLE OF INVENTION: PLANT LESION FORMATION SUPPRESSING GENE, Sp17 AND USE THEREOF
; FILE REFERENCE: 23572-005 NAL
; CURRENT APPLICATION NUMBER: US/10/168,273B
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/JP01/09153
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: JP 2000-318557
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1 LENGTH: 5579
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: genomic DNA
; NAME/KEY: CDS
; LOCATION: (3711)..(3947)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4185)..(5327)

Query Match Similarity 1.6%; Score 28; DB 13; Length 5579;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
US-10-168-273B-1

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;
; LOCATION: (1) .. (630)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_32474C.1
US-10-437-963-27816

Query Match      1.5%; Score 26; DB 17; Length 630;
Best Local Similarity 100.0%; Pred. No. 0.033; Mismatches 0; Indels 0; Gaps 0;
Matches 26; Conservative 0; N mismatches 0; O indels 0; Gaps 0;

Qy   1 ACTTTAGATAAAAGTAAGTCACAA 26
Db   428 ACTTTAGATAAAAGTAAGTCACAA 453

RESULT 6
US-10-425-114-718/C
; Sequence 718, Application US/10425114
; Publication No. US2004003488BA1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; SEQ ID NO: 718
; LENGTH: 858
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700087978_FLI
US-10-425-114-718

Query Match      1.4%; Score 25; DB 13; Length 858;
Best Local Similarity 100.0%; Pred. No. 0.11; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; N mismatches 0; O indels 0; Gaps 0;

Qy   49 ATTTTTATAAGACGAGTGGTCA 73
Db   655 ATTTTTATAAGACGAGTGGTCA 631

RESULT 7
US-10-260-218-2163
; Sequence 2163, Application US/10260238
; GENERAL INFORMATION:
; APPLICANT: Budworth, Paul R.
; APPLICANT: Moughamer, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provost, Nicholas
; APPLICANT: Ruckle, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
; FILE REFERENCE: 60111-NP
; CURRENT APPLICATION NUMBER: US/10/260,238
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/325,448
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; SEQ ID NO: 2
; LENGTH: 3 673 778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; NAME/KEY: US/ture
; FEATURE:

RESULT 8
US-10-437-963-10006/C
; Sequence 10006, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO: 10006
; LENGTH: 6064
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_16369C.1
US-10-437-963-10006

Query Match      1.4%; Score 25; DB 17; Length 6064;
Best Local Similarity 100.0%; Pred. No. 0.13; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; N mismatches 0; O indels 0; Gaps 0;

Qy   91 CTGAAAATTCCCTTATATTATGGGAC 115
Db   3129 CTGAAAATTCCCTTATATTATGGGAC 3105

RESULT 9
US-10-312-841-2
; Sequence 2, Application US/10312841
; Publication No. US20030186227A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des Mi
; FILE REFERENCE: E01/1208/WO
; CURRENT APPLICATION NUMBER: US/10/312,841
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO: 2
; LENGTH: 3 673 778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; NAME/KEY: US/ture
; FEATURE:

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; LOCATION: (379615)
; US-10-312-941-2
Query Match 1.4%; Score 25; DB 15; Length 3673778;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
Db 729897 ATTAAATTAACTTTTTTTTTA 1346
Qy 1322 ATTAAATTAACTTTTTTTTTA 729921

RESULT 10
US-10-437-963-87728
; Sequence 87728, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; CURRENT APPLICATION NUMBER: US/10/437,963
; SEQ ID NO: 86792
; LENGTH: 467
; OTHER INFORMATION: Clone ID: PAT_MRT4530_857C.1
; US-10-437-963-87728

Query Match 1.4%; Score 24; DB 17; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 24; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
Db 87728 ATTAAATTAACTTTTTTTA 359
Qy 309 GATATAAGTAAGTCACAGAAA 332
Db 309 GATATAAGTAAGTCACAGAAA 332

RESULT 11
US-10-424-599-64432
; Sequence 64432, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; CURRENT APPLICATION NUMBER: US/10/437,963
; SEQ ID NO: 64432
; LENGTH: 390
; OTHER INFORMATION: Glycine max
; US-10-424-599-64432

Query Match 1.4%; Score 24; DB 13; Length 390;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 24; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
Db 75 AGAAAAAAACAAACAAACACA 98
Qy 153 AGAAAAAAACAAACAAACACA 176
Db 75 AGAAAAAAACAAACAAACACA 98

RESULT 12
US-10-437-963-86792
; Sequence 86792, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; CURRENT APPLICATION NUMBER: US/10/437,963
; SEQ ID NO: 86792
; LENGTH: 467
; OTHER INFORMATION: Clone ID: PAT_MRT4530_857C.1
; US-10-437-963-86792

Query Match 1.4%; Score 24; DB 17; Length 467;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 24; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
Db 373 TTATATTATGGACGGAGAAGTA 396
Qy 116 TTATATTATGGACGGAGAAGTA 139
Db 373 TTATATTATGGACGGAGAAGTA 396

RESULT 13
US-10-437-963-43365/C
; Sequence 43365, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; CURRENT APPLICATION NUMBER: US/10/437,963
; SEQ ID NO: 43365
; LENGTH: 1480
; OTHER INFORMATION: Glycine max
; US-10-437-963-43365

Query Match 1.4%; Score 24; DB 13; Length 390;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 24; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
Db 204966 ATTAAATTAACTTTTTTTA 390
Qy 1322 ATTAAATTAACTTTTTTTA 390
Db 204966 ATTAAATTAACTTTTTTTA 390

RESULT 14
US-10-437-963-43365
; Sequence 43365, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; CURRENT APPLICATION NUMBER: US/10/437,963
; SEQ ID NO: 43365
; LENGTH: 1480
; OTHER INFORMATION: Glycine max
; US-10-437-963-43365

Query Match 1.4%; Score 24; DB 13; Length 390;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 24; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
Db 204966 ATTAAATTAACTTTTTTTA 390
Qy 1322 ATTAAATTAACTTTTTTTA 390
Db 204966 ATTAAATTAACTTTTTTTA 390

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Query Match Similarity 1.4%; Score 24; DB 17; Length 1480;
 Best Local Similarity 100.0%; Pred. No. 0.37; Mismatches 0; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTTAGATATAAGTAAGTCACAA 26
 Db 1285 TTTAGATATAAGTAAGTCACAA 1262

RESULT 14
 US-10-260-218-1731
 ; Sequence 1731, Application US/10260238
 ; GENERAL INFORMATION:
 ; APPLICANT: Budworth, Paul R.
 ; APPLICANT: Brughamer, Todd G.
 ; APPLICANT: Briggs, Steven P.
 ; APPLICANT: Cooper, Bret
 ; APPLICANT: Glazebrook, Jane
 ; APPLICANT: Goff, Stephen A.
 ; APPLICANT: Katagiri, Fumiaki
 ; APPLICANT: Krebs, Joe
 ; APPLICANT: Provart, Nicholas
 ; APPLICANT: Ricke, Darrell
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
 ; FILE REFERENCE: 60111-NP
 ; CURRENT APPLICATION NUMBER: US/10/260,238
 ; CURRENT FILING DATE: 2002-09-26
 ; PRIOR APPLICATION NUMBER: US 60/325,448
 ; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: US 60/325,277
 ; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: US 60/370,620
 ; PRIOR FILING DATE: 2002-04-04
 ; NUMBER OF SEQ ID NOS: 6077
 ; SEQ ID NO 1731
 ; LENGTH: 2000
 ; TYPE: DNA
 ; ORGANISM: Oryza sativa
 US-10-260-218-1731.

Query Match Similarity 1.4%; Score 24; DB 16; Length 2000;
 Best Local Similarity 100.0%; Pred. No. 0.38; Mismatches 0; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 57 AATAAGACGAGTGTGTCAAACAGTA 80
 Db 1166 AATAAGACGAGTGTGTCAAACAGTA 1189

RESULT 15
 US-10-437-963-4401/C
 ; Sequence 4401, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Borkharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-1-(5321)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; SEQ ID NO 4401
 ; LENGTH: 433



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OM nucleic - nucleic search, using sw model

Run on: October 2, 2004, 05:05:33 ; Search time 11065 seconds
 (without alignments)
 6941.153 Million cell updates/sec

Title: US-10-009-570-1

Perfect score: 1772

Sequence: 1 acttttggataaaatgttaag.....ctcttccttcgtgcaag 1772

Scoring table: Oligo_NUC
 Gapop_60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:
 1: gb_ba: *
 2: gb_htg: *
 3: gb_in: *
 4: gb_on: *
 5: gb_ov: *
 6: gb_dat: *
 7: gb_ph: *
 8: gb_D1: *
 9: gb_pr: *
 10: gb_ro: *
 11: gb_sts: *
 12: gb_sy: *
 13: gb_un: *
 14: gb_vt: *
 15: em_ba: *
 16: em_fun: *
 17: em_hum: *
 18: em_in: *
 19: em_mu: *
 20: em_om: *
 21: em_or: *
 22: em_ov: *
 23: em_pat: *
 24: em_ph: *
 25: em_pl: *
 26: em_ro: *
 27: em_sts: *
 28: em_un: *
 29: em_vt: *
 30: em_htg_hum: *
 31: em_htg_inv: *
 32: em_htg_other: *
 33: em_htg_mus: *
 34: em_htg_pln: *
 35: em_htg_rdn: *
 36: em_htg_mam: *
 37: em_htg_vrt: *
 38: em_sy: *
 39: em_htg_hum: *
 40: em_htg_mus: *
 41: em_htg_other: *

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1772	100.0	1772	6	AX063520	AX063520 Sequence
2	1772	100.0	1803	6	AX063522	AX063522 Sequence
3	1686	95.1	1686	6	AX063525	AX063525 Sequence
4	947	53.4	168173	8	AP004988	Oryza sat
5	660	37.2	2000	6	AX656635	AX656635 Sequence
6	86	4.9	86	6	AX063523	AX063523 Sequence
7	55	3.1	2771	8	AK103036	AK103036 Oryza sat
8	52	2.9	139653	2	AP005890	Oryza sat
C 9	52	2.9	163555	2	AP005912	Oryza sat
C 10	50	2.8	135594	8	AC087220	Oryza sat
C 11	48	2.7	124366	8	AC131374	Oryza sat
C 12	48	2.7	150465	8	AC091749	Oryza sat
C 13	48	2.7	300029	8	AE01776	Oryza sat
C 14	45	2.5	2000	6	AX656219	AX656219 Sequence
C 15	45	2.5	4817	2	AF244558	Oryza sat
C 16	45	2.5	139043	2	AC090974	Oryza sat
C 17	45	2.5	183580	8	AP003561	Oryza sat
C 18	44	2.5	137852	8	AP003880	Oryza sat
C 19	40	2.3	127506	8	OSJN0096	OSJN0096
C 20	40	2.3	167269	8	OSJN0095	OSJN0095
C 21	38	2.1	112483	2	AP004060	AP004060
C 22	38	2.1	132151	8	AC120533	AC120533 Oryza sat
C 23	38	2.1	149807	2	AP004750	AP004750 Oryza sat
C 24	38	2.1	151517	2	AP004491	AP004491 Oryza sat
C 25	38	2.1	158291	2	AP004776	AP004776 Oryza sat
C 26	38	2.1	159290	2	AP004813	AP004813 Oryza sat
C 27	38	2.1	160562	2	AP005613	AP005613 Oryza sat
C 28	38	2.1	168430	8	AC126221	AC126221 Oryza sat
C 29	37	2.1	15815	8	AP003105	AP003105 Oryza sat
C 30	37	2.1	164583	8	AP003197	AP003197 Oryza sat
C 31	36	2.0	106052	2	AC134933	AC134933 Oryza sat
C 32	36	2.0	135670	8	AP005002	AP005002 Oryza sat
C 33	36	2.0	152058	8	AP005740	AP005740 Oryza sat
C 34	36	2.0	175447	2	AC136956	AC136956 Oryza sat
C 35	36	2.0	180544	2	AC137623	AC137623 Oryza sat
C 36	35	2.0	121388	8	AP003759	AP003759 Oryza sat
C 37	35	2.0	127506	8	OSJN0096	OSJN0096
C 38	35	2.0	133800	8	AP004801	AP004801 Oryza sat
C 39	35	2.0	139482	2	AC113333	AC113333 Oryza sat
C 40	35	2.0	149646	2	AP003761	AP003761 Oryza sat
C 41	35	2.0	159626	8	AP005803	AP005803 Oryza sat
C 42	35	2.0	173522	8	OSJN0060	OSJN0060
C 43	34	1.9	2000	6	AC656261	AC656261 Sequence
C 44	34	1.9	131184	8	AP003868	AP003868 Oryza sat
C 45	34	1.9	135014	8	AP003222	AP003222 Oryza sat

ALIGNMENTS

RESULT 1	AX063520	AX063520 Sequence 1 from Patent	1772 bp	DNA
LOCUS		AX063520 Sequence 1 from Patent	W00078975.	
DEFINITION		AX063520		
ACCESSION				
VERSION	AX063520.1	GT:12541259		
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
			PAT 24-JAN-2001	
			linear	
				DANISCO A/S (DK)

FEATURES	Location/Qualifiers	
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/organism	"synthetic construct"	
/mol_type	"unassigned DNA"	
/db_xref	"taxon:32630"	
/note	"promoter sequence"	
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Db	1 ACTTGTAGATAAACTAAAGTCACAGAAAATAATAAATATTCCAAATTTTATAA 60	
Qy	61 AGACGAGTGGTCAACACAGTAAAGTCAAAGTAAACTCRAAAATTCCCTTAATTACGGACTTAA 120	
Db	61 AGACGAGTGGTCAACAGTAAAGTCAAAGTAAACTCRAAAATTCCCTTAATTACGGACTTAA 120	
Qy	121 TTATGGACGGAAAGTAGAAGATGTGAGCAAGAAAAAACACACCGC 180	
Db	121 TTATGGACGGAAAGTAGAAGATGTGAGCAAGAAAAAACACACCGC 180	
Qy	181 CACCTGGCAGGGATGATCATTTAGTCGCAATTGGAGGTGAGAGTTAC 240	
Db	181 CACCTGGCAGGGATGATCATTTAGTCGCAATTGGAGGTGAGAGTTAC 240	
Qy	241 CTACACAACCTGCTTCCTICAGTGAGGTGATGTTCTGCTGCAATTGCGG 300	
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Qy	361 GAGAAAACCGGGCTGGAGCAAGGAGCTAACCTTCACTGAAAGGCTGA 420	
Db	361 GAGAAAACCGGGCTGGAGCAAGGAGCTAACCTTCACTGAAAGGCTGA 420	
Qy	421 ACCCATCTGCCAAATCCGCAATTGCGATTGTTGTTCAATTCCAACCTTGCACTTCCCTTCAGATTG 480	
Db	421 ACCCATCTGCCAAATCCGCAATTGCGATTGTTGTTCAATTCCAACCTTGCACTTCCCTTCAGATTG 480	
Qy	481 GTTGCACTTCAACCGTAGTACATCTGAALAAATGACTGTAAATCCCTGAAAGACCT 540	
Db	481 GTTGCACTTCAACCGTAGTACATCTGAALAAATGACTGTAAATCCCTGAAAGACCT 540	
Qy	541 TCACTGGAGCATGCCCTGCAGGGATTAGCTTAAGAAAATAATAATGACTTTCAGTTGAA 600	
Db	541 TCACTGGAGCATGCCCTGCAGGGATTAGCTTAAGAAAATAATAATGACTTTCAGTTGAA 600	
Qy	601 ACTTAAATTGCAAGTTGAGTTTCACTGGTTCCATGTAAGTGTAAATTCTACTATGCA 660	
Db	601 ACTTAAATTGCAAGTTGAGTTTCACTGGTTCCATGTAAGTGTAAATTCTACTATGCA 660	
Qy	661 GTTTAACCGCTTAATGCTAGTATAAAATTCTATAGTCAATTAAATCATTT 720	
Db	661 GTTTAACCGCTTAATGCTAGTATAAAATTCTATAGTCAATTAAATCATTT 720	
Qy	721 TAGTGTGCTTCAATTTCATGACCTATGACATTGACAA 780	RESULT 2
Db	721 TAGTGTGCTTCAATTTCATGACCTATGACATTGACAA 780	AX063522 AX063522
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Db	781 TAAAAGTTAACTAAAGCACTCGCTCATCAACACCCAAACGTCACCGATGGTGCCTCTC 840	DEFINITION AX063522 AX063522
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Db	841 GACCACGAGTTAGCACTGTGCAACATATAATGCGTGGATGAAACATCTACTGTGGGC 900	KEYWORDS synthetic construct
		ORGANISM synthetic construct
		ARTIFICIAL SEQUENCES artificial sequences.
AUTHORS	Donaldson, I. A. and Rasmussen, T.B.	1
	Rice sucrose synthase promoter	Rice

JOURNAL	Patent: WO 0078975-A-3 28-DEC-2000;
FEATURES	DANISCO A/S (DK)
source	Location/Qualifiers 1. .1803 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:2630" /note="nucleic acid sequence"
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Qy	1 ACTTTAGATAATAAAGTAACTGCAAGAAAATAATAATTAATTCCAAATTTTTAATA 60
Db	1 ACTTTAGATAATAAAGTAACTGCAAGAAAATAATAATTAATTCCAAATTTTTAATA 60
Qy	61 AGACGAGTGTCTAACAGTACAAGTAAACACTCAAATTCTPATATATGGACTTATA 120
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Qy	121 TTATGGACCGGAGGAAGTAGAAAGATTGTAGCCCAGAAAAACAAAAACACCCG 180
Db	121 TTATGGACCGGAGGAAGTAGAAAGATTGTAGCCAAACAAAAACACCCG 180
Qy	181 CACCTGGCAGGCATGTCATCTTAGTCGGCACATGAGAGGTGCAATTGAGTTAC 240
Db	181 CACCTGGCAGGCATGTCATCTTAGTCGGCACATGAGAGGTGCAATTGAGTTAC 240
Qy	241 CTACACAATGCTCTTCAGTGACTGAGCTGAGGTGCAATTGAGTTACATTGAGG 300
Db	241 CTACACAATGCTCTTCAGTGACTGAGCTGAGGTGCAATTGAGTTACATTGAGG 300
Qy	301 CAGCAGCTGAAACAGTGTGAGAACATCGATAATTGTCAGGGAGAAACATG 360
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Qy	361 GAGAAAACCGGGACTGGAGACGGACGAACTGAGCTTCAATTGAGATG 420
Db	361 GAGAAAACCGGGCTGGAGACGGACGAACTGAGCTTCAATTGAGGCTG 420
Qy	421 ACCCATCTGGAATTCGZGAATGGTTGTTCAATTCAACTGAGCTTCAATTG 480
Db	421 ACCCATCTGGAATTCGZGAATGGTTGTTCAATTCAACTGAGCTTCAATTG 480
Qy	481 GTTCATGTTCAACCGTAACTACATCTGAAATAATGCTTAATACCTTGAGAGACT 540
Db	481 GTTCATGTTCAACCGTAACTACATCTGAAATAATGCTTAATACCTTGAGAGACT 540
Qy	541 TCACTGGGAGCTGCTGCAAGGCATTAGCTTAAGGAAAATAATAATGCTTTCGAA 600
Db	541 TCACTGGGAGCTGCTGCAAGGCATTAGCTTAAGGAAAATAATAATGCTTTCGAA 600
Qy	601 ACTTAATTTGGGTTAGATTAGGGTTCCATCGTAGTGTATTCTACTATGCA 660
Db	601 ACTTAATTTGGGTTAGATTAGGGTTCCATCGTAGTGTATTCTACTATGCA 660
Qy	661 GTTTAAACCGCTAAATGTCGATAATAAATTTCATCTAGCATTTATAATCATT 720
Db	661 GTTTAAACCGCTAAATGTCGATAATAAATTTCATCTAGCATTTATAATCATT 720
Qy	721 TAGTTGCTGTCATTTCGTTACCACTTCAACCATGCTCACTGATCAATTGACA 780
Db	721 TAGTTGCTGTCATTTCGTTACCACTTCAACCATGCTCACTGATCAATTGACA 780
Qy	781 TAAGAGTACTAACGACATGCTCATCACACCAAGCTCACGATGGTGCCTCTC 840
Db	781 TAAGAGTACTAACGACATGCTCATCACACCAAGCTCACGATGGTGCCTCTC 840
Qy	841 GACCAAGAGTTAACGTTACACTGTCGAAACATATGCGTGCATGACATCTGCGCC 900
Db	841 GACCAAGAGTTAACGTTACACTGTCGAAACATATGCGTGCATGACATCTGCGCC 900
RESULT 3	AX063525
LOCUS	Sequence 6 from Patent WO0078975.
DEFINITION	AX063525
ACCESSION	AX063525.1 GI:12541264
VERSION	synthetic construct
KEYWORDS	synthetic construct
ORGANISM	artificial sequences.
REFERENCE	1

REFERENCE	1	Sasaki,T., Matsumoto,T. and Yamamoto,K. Oryza sativa nippobore (G33) genomic DNA, clone B1056G08 chromosome 7, BAC	gene	NPFIAEFLCCNLCGYPLAGRSPFIYIGEKAFCKBECRSYVVEAREREKRA AAAAAAASPEKKKEAAAKRGGBECRECSIFFCADDI"
AUTHORS		complement (join(5482 . 5716, 6013 . 6023))	mRNA	/gene=B1056G08..102"
TITLE		complement (join(5482 . 5716, 6013 . 6023))	misc_feature	/note="hypothetical ORF predicted by GENSCAN this category is not included in IRGSP standard"
JOURNAL		join(7413 . 7432 . 7688 . 8096)	gene	/gene=B1056G08..102"
REFERENCE	2	(bases 1 to 168173) Sasaki,T., Matsumoto,T. and Yamamoto,K. Direct Submission	mRNA	/note="hypothetical ORF predicted by GENSCAN this category is not included in IRGSP standard"
AUTHORS		join(7413 . 7432 . 7688 . 8096)	gene	/gene=B1056G08..102"
TITLE		join(7413 . 7432 . 7688 . 8096)	mRNA	/note="hypothetical ORF predicted by GENSCAN this category is not included in IRGSP standard"
JOURNAL		join(7413 . 7432 . 7688 . 8096)	misc_feature	/note="hypothetical ORF predicted by GENSCAN this category is not included in IRGSP standard"
COMMENT		Submitted (27-MAR-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai (B-mail:tssasaki@affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/, Tel:81-298-32-7441, Fax:81-298-38-7468) On Oct 16, 2002 this sequence replaced gi:22212589. Genes were predicted from the integrated results of the following: GENSCAN (http://CCR-081.mit.edu/GENSCAN.html), FGENESH (http://www.softberry.com/), GeneMark.hmm (http://opal.biology.gatech.edu/GeneMark/), GlimmerM (http://www.tigr.org/db/glimmer/glimmer_form.html), RICEHMM (http://bioinformatics.iastate.edu/cgi-bin/RICEHMM/), spliceredictor (http://globin.cse.psu.edu/html/docs/sim.html), gap2 (http://www.tigr.org/software/glimmerm/), BLASTN and BLASTX. The genomic sequence was searched against NCBI NonRedundant Protein database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the CDNA sequence database at RGP or dbJU. Protein homologues of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP. ESTs represent the identified cDNA sequences using BLASTN with the corresponding DBJU accession no. and RGP clone ID. Full-length cDNAs represent the identified cDNA sequences using BLASTN with the corresponding DBJU accession no. A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with full-length cDNA or EST homology (covering almost the entire length of Partial sequence) is classified as an 'unknown' protein. A gene predicted by two or more gene prediction programs is classified as a 'hypothetical' protein according to IRGSP standard. A gene predicted by a single gene prediction program is also classified as a probable 'hypothetical' protein and is included as a miscellaneous feature of the sequence.	gene	/note="hypothetical ORF predicted by GENSCAN this category is not included in IRGSP standard"
FEATURES		The orientation of the sequence is from M13rev to -M13 of the BAC clone. This is a partial sequence of B1056G08 clone. This sequence of B1056G08 clone has an overlap with P0552F09 clone (DBJ: AP005198) at 5' end and an overlap with P05608 clone (DBJ: AP004308) at 3' end and an overlap with P05608 clone (DBJ: AP004309) at 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html.	mRNA	/note="hypothetical ORF predicted by GENSCAN this category is not included in IRGSP standard"
source		Location/Qualifiers 1..168173	gene	/note="hypothetical ORF predicted by GENSCAN this category is not included in IRGSP standard"
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		/db_xref="Taxon:39947"	mRNA	/note="putative transposase" join(11828 .. 11934,12176 .. 12278,12484 .. 14473 .. 14478 , /gene=B1056G08..106-1"
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		complement (3083 . 4070)	gene	/note="putative transposase" join(11828 .. 11934,12176 .. 12278,12484 .. 14473 .. 14478 , /gene=B1056G08..106-1"
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		/note="supported by full-length cDNA(s): AK108210"	mRNA	/note="putative transposase" join(11828 .. 11934,12176 .. 12278,12484 .. 14473 .. 14478 , /gene=B1056G08..106-1"
		complement (join(3286 . 3490, 3648 . 4036))	gene	/note="putative transposase" join(11828 .. 11934,12176 .. 12278,12484 .. 14473 .. 14478 , /gene=B1056G08..106-1"
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		/translation="MASAVVAKPPAAPASRRRCFVERAAAAGVNAAIAAVDDH RPVPAAAAAMDDUVGRVARPARPSARAIMEGTHQLISSGGYCTVPNCSTGN	mRNA	/note="putative transposase" join(11828 .. 11934,12176 .. 12278,12484 .. 14473 .. 14478 , /gene=B1056G08..106-1"

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 join(21538. .21596,1679. .21858. .22064,22185. .22240,
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 CNQKKSIAPTVHSRSERTVSGYANRNLNPQPLAOVNPNAFDLKENRTPEAGSILRA
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 QEEDEPDETDKBEYESIENEURSPADESSENFGI.SHEFGNSDGPSENQDYSFSPS
 DAPIPLGGSKENAFAGNEMHDTPEGEVDAWSMSPRPHLFAYANDNSDGAFAISSPGSPW
 NISHTDQUDLTDVSRMKCKWQSQAFPVGNAQDFKFLKKEFGKTRKGAD
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 /note="supported by full-length cDNA(s) : AK064501"
 29193. .31064

mrna
 misc_feature
 note="supported by full-length cDNA(s) : AK064501"

Query Match	Score	Length	Best Local Similarity	Start	End	Matches	Conservative	Indels	Gaps	note
Qy 7 GATAATAAGTAAGTCACAAGAAAAATAATAATTCCAATTTTAATAAGAGA	53.4%	947	DB 8 ;	168173;		67	67	0;	3 ;	/gene="B105G08.108"
Db 67444 GATAATAAGTAAGTCACAAGAAAAATAATAATTCCAATTTTAATAAGAGA	53.4%	67503	Db 9	168173;		67	67	0;	3 ;	/note="supported by full-length cDNA(s) : AK064501"
Qy 127 GACGGAGGAAGTAGAAATTTGAGCCATTACATGGCCACCTTG	53.4%	186	Db 10	168173;		67554	67554	0;	3 ;	mrna
Db 67554 GATGGAGGAGTAGAAATTTGAGCCATTACATGGCCACCTTG	53.4%	67623	Db 11	168173;		67504	67504	0;	3 ;	misc_feature
Qy 187 GCGGGCATGCATCTTACGTGGCAATTAGAGCTGGTACCCCTAAC	53.4%	246	Db 12	168173;		67624	67624	0;	3 ;	note="supported by full-length cDNA(s) : AK064501"
Db 67624 GCGGGCATGCATCTTACGTGGCAATTAGAGCTGGTACCCCTAAC	53.4%	67683	Db 13	168173;		67683	67683	0;	3 ;	note="supported by full-length cDNA(s) : AK064501"
Qy 247 AACCTGCTTCTCAGTGGACCTAGCTGGCATGTTCTGCAATTACATG	53.4%	306	Db 14	168173;		67684	67684	0;	3 ;	note="supported by full-length cDNA(s) : AK064501"
Db 67684 AGCTGCTTCTCAGTGGCATGTTCTGCAATTACATG	53.4%	67743	Db 15	168173;		67743	67743	0;	3 ;	note="supported by full-length cDNA(s) : AK064501"
Qy 307 CTAGCAAATGGTTCAGGAAACATCGATAATCGATAATCGGAGAAA	53.4%	366	Db 16	168173;		67744	67744	0;	3 ;	note="supported by full-length cDNA(s) : AK064501"
Db 67744 CTAGCAAATGGTTCAGGAAACATCGATAATCGGAGAAA	53.4%	67803	Db 17	168173;		67744	67744	0;	3 ;	note="supported by full-length cDNA(s) : AK064501"
Qy 357 AACGGGGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	53.4%	426	Db 18	168173;		67803	67803	0;	3 ;	note="supported by full-length cDNA(s) : AK064501"
Db 67803 AACGGGGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	53.4%	67883	Db 19	168173;		67883	67883	0;	3 ;	note="supported by full-length cDNA(s) : AK064501"
Qy 1444 GAACAGATATTAGTGCACAGACAATGCCAACATGGAGGAGGAGG	53.4%	1503	Db 20	168173;		1444	1444	0;	3 ;	note="supported by full-length cDNA(s) : AK064501"

JOURNAL	Published Only in Database (2002)	FEATURES	* the accession number will be preserved.
AUTHORS	2 (bases 1 to 139653)	source	1. 1.163555
TITLE	Direct Submission		/organism="Oryza sativa (japonica cultivar-group)"
JOURNAL	Submitted (13-NOV-2002) Takaji Sasaki, National Institute of		/mol_type="Genomic DNA"
	Agrobiological Sciences, Rice Genome Research Program; Kannondai		/cultivar="Nipponbare"
	2-1-2, Tsukuba, Ibaraki 305-8602, Japan		/db_xref="Taxon:39947"
	(E-mail:tsasaki@niasaffrc.go.jp, URL:http://rgp.dna'affrc.go.jp/		/chromosome="9"
	Te1:81-298-38-7441, Fax:81-298-38-7468)		/clone="OSJNBB0064123"
COMMENT	NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.	ORIGIN	
	* NOTE: This is a 'working draft' sequence.	Query Match	2.9%; Score 52; DB 2; Length 163555;
	* This sequence will be replaced by the finished sequence as soon as it is available and	Best Local Similarity	100.0%; Pred. No. 3.3e-16;
	* the accession number will be preserved.	Matches	52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
FEATURES	Location/Qualifiers	Qy	28 AAAATAATATAATTCCAAATTTTAATAGACGAGTGTCAAAAGT 79
	1..139653	Db	55781 AAAATAATATAATTCCAAATTTTAATAGACGAGTGTCAAAAGT 55730
	/organism="Oryza sativa (japonica cultivar-group)"	RESULT	10
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	/cultivar="Nipponbare"	LOCUS	Oryza sativa chromosome 3 BAC OSJNBB0097F01 genomic sequence,
	/db_xref="Taxon:39947"	DEFINITION	complete sequence.
	/chromosome="9"	AC087220	AC087220.9 GI:28460790
	/clone="B1039C06"	VERSION	HTG.
		KEYWORDS	Oryza sativa (japonica cultivar-group)
		SOURCE	Eukaryota; Viridiplantae; Streptophytta; Embryophytta; Tracheophytta; Spermatophytidae; Oryzeidae; Oryzae.
		ORGANISM	1 (bases 1 to 135594)
		REFERENCE	Buell,C.R., Yuan,Q., Ouyang,S., Liu,J., Gansberger,K., Jones,K.M., Overton,T., Tisbiran,T., Kim,M.M., Bera,J.J., Jin,S.S., Padrosh,D.W., Tallon,L.J., Koo,H., Zismann,V., Hsiao,J., Blunt,S., Vanaken,S.S., Riedmiller,S.B., Utterback,T.T., Feldblyum,T.V., Yang,Q.Q., Haas,B.J., Sub,B.B., Petersen,J.J., Quackenbush,J., White,O., Salzberg,S.L. and Fraser,C.M.
		AUTHORS	Unpublished
		JOURNAL	Oryza sativa chromosome 3 BAC OSJNBB0097F01 genomic sequence
		REFERENCE	2 (bases 1 to 135594)
		AUTHORS	Direct Submission
		JOURNAL	Submitted (15-DBC-2000) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA
		REFERENCE	3 (bases 1 to 135594)
		AUTHORS	Direct Submission
		JOURNAL	Submitted (21-FEB-2003) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA
		REFERENCE	4 (bases 1 to 135594)
		AUTHORS	Buell,R.
		JOURNAL	Direct Submission
		REFERENCE	Submitted (12-MAR-2003) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA
		AUTHORS	On Feb 21, 2003 this sequence version replaced gi:16418178.
		JOURNAL	Address all correspondence to rice@tigr.org
		COMMENT	BAC clone OSJNBB0097F01 is from Oryza sativa chromosome 3
			The orientation of the sequence is from SP6 to T7 end of the BAC clone.
			Genes were identified by a combination of several methods: Gene prediction programs including Genescan (http://www.softberry.com/), Genescan and Genescan+ (Chris Burge, http://CCR-081.mit.edu/SENSCAN.html), GeneMarkMM (Mark Borodovsky, http://genemark.biology.gatech.edu/GeneMark/), and GeneSplicer (Mihalea Perrea and Steven Salzberg, Contact mperrea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/cdb/tgi.shtml).
			Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named
JOURNAL	Sasaki,T., Matsumoto,T. and Katayose,Y.		
AUTHORS	Oryza sativa nipponbare (GA3) genomic DNA, chromosome 9, BAC		
TITLE	clones:OSJNBB0064123		
JOURNAL	Submitted Only in Database (2002)		
REFERENCE	2 (bases 1 to 163555)		
AUTHORS	Sasaki,T., Matsumoto,T. and Katayose,Y.		
TITLE	Submitted (21-NOV-2002) Takaji Sasaki, National Institute of		
JOURNAL	Agribiological Sciences, Rice Genome Research Program; Kannondai		
	2-1-2, Tsukuba, Ibaraki 305-8602, Japan		
	(E-mail:tsasaki@niasaffrc.go.jp, URL:http://rgp.dna'affrc.go.jp/		
	Te1:81-298-38-7441, Fax:81-298-38-7468)		
COMMENT	NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.		
	* NOTE: This is a 'working draft' sequence.		
	* This sequence will be replaced by the finished sequence as soon as it is available and		

after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, <http://genome.wustl.edu/eddy/tRNAscan-SE/>). Simple repeats are identified by repeatmasker (Arian Smit, <http://ftp.genome.washington.edu/RM/RepeatMasker.html>).

This BAC overlaps with rice BAC OSJNBA0013M12 (AC082644) and OSJNBA0090L05 (AC084765).

Location/Qualifiers

FEATURES	source		CDS	complement(join(6551..6928,7019..7198,7813..8808))
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	/protein_id="AA062323.1"		/db_xref="GI:28927677"	/translation="MTDVMRACAVSRNRHGLGARPVVLRFCLHDFFSROEKLDRLA FVNLLARADDGTTSTVVEELTSKLEPLNRSQRMSGRVPSVDAQUDAWQYGM QHRSKSFTQLQNYMLPLNURNSNSNGCQVNLKMTGGATRILSMVLSNKA CLRLPNTWLTSDLVHLTDEDDLNQIESTAROPSLSRKLCIHKOTSPATTDDOSLH LESNBLLKVSLSWLTWSRALYLVELETRPTECHDNQTCRCKEPLQFLTLHLTTQKD ASTYQDVENDPCVRLFETENISSLRPECDHNQTCRCKEPLQFLTLHLTTQKD GHDSABEVELJKDIDOLPHATSLSLQVOFAQYDITASVLCULTRCKPLKHLBLNITYKM AEYCKRPQIGTONQDRHILSLERLOQKITSAYKROYCVRBLKLHISAPALKM VAFISAFLMSQSLQCAKECEFLHSIPLNEKGWAFYHGAIHQDFTFEWTDJKV ECRQVHMD"
	10607..12644		/gene="OSJNBB0097F01.4"	/note="predicted by fgenesh"
	/db_xref="GI:28927677"		join(<10607..10874,11173..>12644)	/note="predicted by fgenesh"
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	/join(<15195..15291,15955..16184,16327..16585, 16680..>17351)		/codon_start=1	
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	16421..16448		/repeat_region	
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	/rpt.family="(G)n"		/repeat_region	
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Query Match	2.8%	Score 50; DB 8; Length 135594;	/note="Contains similarity to receptor-like protein kinase"		
Best Local Similarity	100.0%	Pred. No. 4e-15; Mismatches 0; Indels 0; Gaps 0;	complement (join(6525..6842, 6942..7095, 7308..7545, 7116..7926, 7998..8122, 9335..9443, 9532..9772, 11989..12084, 13110..13229, 13335..14193))		/gene="OSJNAb0008A05.2"
Matches 50;	Conservative 0;		/codon_start=1		/product="Putative receptor-like protein kinase"
Qy	7	GATAATAAGTAACTCACAGAAAATAATAATTCAATTCTTTTTT 56	/protein_id="AAN04149.1"		
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AC131374	AC131374	124366 bp DNA linear PLN 03-SEP-2002	repeat_region	16903..16930	/note="Simple Sequence Repeat (ATAG)n"
LOCUS	OSJNAb0008A05	(japonica cultivar-group) chromosome 10 clone	repeat_region	16931..23213	/note="Similar to transposon"
DEFINITION	AC131374	complete sequence	repeat_region	23214..23321	/note="Similar to transposon"
ACCESSION	AC131374		gene		
KEYWORDS	HTG.		complement (23976..23976)		
SOURCE	Oryza sativa	(japonica cultivar-group)	complement (join(23976..23976))		
ORGANISM	Oryza sativa	(japonica cultivar-group)	gene	"OSJNAb0008A05.3"	
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			complement (join(23976..23976))		
REFERENCE	1	(bases 1 to 124366)	gene	"OSJNAb0008A05.3"	
AUTHORS	Wing, R.A., Yu, Y., Soderlund, C., Kim, H.-R., Rambo, T., Sasaki, C., Currie, J. and Collura, K.		/codon_start=1		
TITLE	Rice Genomic Sequence		/product="Putative polyprotein"		
JOURNAL	Unpublished		/protein_id="AAN04150.1"		
REFERENCE	2	(bases 1 to 124366)	/db_xref="GI:22655733"		
AUTHORS	Wing, R.A., Yu, Y., Soderlund, C., Kim, H.-R., Rambo, T., Sasaki, C., Currie, J. and Collura, K.		/translation="MONTRENGNGPNNNNNNGNPIPLAQVLAQQAQLMMQQQL NQQNQGRNHAAPQNKLAEFLRVRPPIFSSTNPVEAGDWLIAEKUDLLOCTDQENV SPASHOLGHGPASEMWDFHFRALRRTAIPITLQFLTAFRKVTRPPIPSGVUSLKEKEFRPG KELEGANDLSYPLMGDQYDFQKNDKDFQKNDKDFQKNDKDFQKNDKDFQKNDKDFQKNDKDFQ PRLTGQSPMPPGSLSVVRFORQFNNNAGNIRNQAPRVAASOOPQPKRERHSSK PVCFCNGDGHADCPKPKRVKVPPKRSATHFELSMSPAGHNMEEVEDLRPMVSTSNOLSLQRPS TELNVLPATMFLDSGATHFELSMSPAGHNMEEVEDLRPMVSTSNOLSLQRPS VRIEQVPLFLNILLSKOLDVIGMDWLARHKVYIDCANRKVLTNSDGRVVTVA ALSESURSRNQITBEPIVREYDPPDOLPGKPKRIDEFLVGGTIPRPIHTRP YRMAANELAEVKRNDLLOGYIRESPPSGAPVIFVEKDHTOMCVYRBLADNTV IKNKLLPDDFLDQKGAVFSKDLRSGHQLRKTEDPKIAFTTRIGLFKCV MSFGLTNTMAPFPMLNPKVMPYDKEFVVFVTTDILYSEBFHLRLAELKE HOLYAFSKCCEFWLSVSKFQGHVISAGGVADPSNVBSVNTWKOPKTVSEFSELGLA GYKKBECQSFQELKNLISAPILLPPDKKGQFQVCDASLGJGQMLQDGKVYA YASRQRPHENYKYPHTDLELAIVHAKNYPHTDLELAIVHAKNYPHTDLELAIVHAK MRORRMLELIKDYDMGLHYHQKGANVYADALSRKGKCNATASGRQPLIECEFERINL GIVSRGEVALEAKPFLIDQVREQAINDPQIKNQMRKGKAIGPLEBQGTWLGJ RSCPVDPNKDLKDALKEAHDTLYSINGSTGQYDQKLERFWMRKEIAFYAVACDV CORVRAEHQKDLQALIOPKLPEWKHEIGMDFTGUPRTSGHDLSIWIVDRLTKVAH FILPKVTYSSSRBLAELYMARLVCIGHLWPKTVKTDSSQFENMKLQEMGSKLNS TAYHPQTDGQPTVQNLDMRLRACDFGGSWDQNLPYAOFSYNNSYQASLQMAYFE ALYGRCRCTPLWDOCTGEROVOEGTDLRBAEKVQLIQBRLRVAGSRKSYADNRD LSPEEGDYYTRVTPFPERCHRFHTGKLLARPPGPKIVSRGEVAYQELPQSLAGV QWSNRHSEBESTWEREDEBLKASPHPLFASSSESRGRDSV"		
FEATURES	1..124366	/organism="Oryza sativa" ('japonica cultivar-group)' /mol_type="genomic DNA" /sub_species="('japonica' cultivar-group)"	/note="Contains similarity to 9PSBY-type retrotransposon protein"	complement (28587..30710)	
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repeat_region				
gene				
CDS				
Query Match		2.7%	Score 48; DB 8; Length 124366;	
Best Local Similarity		100.0%	Pred. No. 4.9e-14;	
Matches		48;	Conservative 0; Mismatches 0;	
			Indels 0; Gaps 0;	
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CDS				
FEATURES				
source				
This BAC overlaps with rice BAC OSJNb00073L20.				
Location/Qualifiers				
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/organism="Oryza sativa (japonica cultivar-group)"				
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http://ftp.genome.washington.edu/RM/RepeatMasker.html				

PLN 06-JUN-2003

AE017076 DNA linear chromosome 10, section 30 of
LOCUS Orzya sativa (japonica cultivar-group) 300029 bp of the complete sequence.
DEFINITION 77 of the complete sequence.

AE017076 AE016959

AE017076.1 GI:31431167

ORGANISM Ehrhartoideae; Orzaeae; Orzya; Poales; Poaceae;
Liliopsida; Magnoliopsida; Streptophyta; Embryophyta; Tracheophyta;
Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

KEYWORDS .
SOURCE .
ORGANISM .
REFERENCE .
AUTHORS The Rice Chromosome 10 Sequencing Consortium
TITLE In-depth view of structure, activity, and evolution of rice
chromosome 10

JOURNAL Science 300, 1566-1569 (2003)

REFERENCE 2 (bases 1 to 300029)
AUTHORS Buell, C.R., Wing, R.A., McCombie, W.R., Messing, J. and Yuan, Q.

TITLE Direct Submission (05-MAY-2003)

JOURNAL The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA

COMMENT This is the pseudomolecule for rice chromosome 10, which was constructed by resolving discrepancies between overlapping BACs, trimming the overlap regions, and linking the unique sequences to form a contiguous sequence. Genes in individual BAC clone were identified by a combination of several methods: Gene prediction programs, searches of the complete sequence against a peptide database and EST databases. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, <http://genome.wustl.edu/eddy/tRNAscan-SE/>).

FEATURES Location/Qualifiers

source

1. . 300029 /organism="Orzya sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="Taxon:39947"
/chromosome="10"

mRNA <1..90733 /note="Chromosome 10 sequence derived from BAC clone OSUNBA0093I09 in this region was derived from BAC clone OSUNBA0093I09 (GB:AC09416)."
<1538..>2977 /locus_tag="OSUNBA0093I09_20"
/note="Therapeutic protein with F box domain"

CDS <1538..>2977 /locus_tag="OSUNBA0093I09_20"
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/product="hypothetical protein"
/protein_id="AA52983_1"
/db_xref="GT:31431168"
/translation="MSSPPPPPPCPAAACDDGWLISVSTYSGESNQKRLKRGGCGG
RKGPGGGAVEDGCPHDEVLLVFAECLTCCRWRWVAGDAEYLICR
RKPPSERVGAVALGVYQOQRDQENNSGAPPPEPFLPSPSYSSREGAFLKVDY
SCILSNSRLISRKIGELVTELRSSPAAYAVLUVCNMBMTDMATLPLLAGDKRPGHY
CAITPDHESAPDRUGFHDPAFVTKRNRFCRSWSDTKAWDGFLKSLSEA
KIGGRGLGEMTGAVAVYGSFVNKLQFLVYRGLAKTATFEPKMSKULCFCYGS
VNRQLAVTPGGRLCAVOVDRAHTSVNTVRNIVNLSHSDGYCPTWEDNARDVLFNRY
LPMLNRRVRCRQGVCEASGVVLAIGTDSLQDPIALYALMDRCRARKVAPPGHC
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complement(<11385..>174721)
/note="Contains Pfam domain pkinase protein kinase domain of e value 7.e-47; contains Pfam domain DUF26 Domain of e value 7.e-10"

gene

			ORGANISM	Oryza sativa
			Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
			Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	
			Ehrhartoidae; Oryzeae; Oryza.	
		REFERENCE	1	
	AUTHORS	Chang, H. S., Chen, W., Cooper, B., Glazebrook, J., Goff, S. A., Hou, Y. M., Katagiri, F., Quan, S., Tao, Y., Whitham, S., Xie, Z., Zhu, T., and Zou, G.		
	TITLE	Plant genes involved in defense against pathogens		
	JOURNAL	Plant		
	FEATURES	Patent: WO 0300898 A 6089 03-JAN-2003;		
	source	Syngenta Participation AG (CH)		
	Location/Qualifiers	1. 2000		
		/organism="Oryza sativa"		
		/mol_type="unassigned DNA"		
		/db_xref="taxon:4530"		
	ORIGIN	Query Match		
		Best Local Similarity 100.0%; Pred. No. 3_5e-12;		
	Matches	Mismatches 0; Indels 0; Gaps 0;		
	Qy	46 CAATTTTTTAATAAGCAGCTGTCAAACAGTACAATTTAA 90		
	Db	294 CAATTTTTTAATAAGCAGCTGTCAAACAGTACAATTTAA 250		
	RESULT 15	AP254558/c		
	LOCUS	AP254558 4817 bp DNA linear PLN 11-MAR-2001		
	DEFINITION	Oryza sativa NAC6 (NAC6) gene, complete cds.		
	ORGANISM	AP254558		
	ACCESSION	AP254558.1 GI:13272280		
	VERSION			
	KEYWORDS	Oryza sativa (japonica cultivar-group)		
	SOURCE	Oryza sativa (japonica cultivar-group)		
	ORGANISM	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
		Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
		Ehrhartoidae; Oryzeae; Oryza.		
	REFERENCE	1 (bases 1 to 4817)		
	AUTHORS	Yoon, U.-H., Hahn, J.-H., and Eun, M.-Y.		
	JOURNAL	Molecular cloning of NAC6 gene in rice		
	REFERENCE	Unpublished		
	AUTHORS	2 (bases 1 to 4817)		
	JOURNAL	Yoon, U.-H., Hahn, J.-H., and Eun, M.-Y.		
	FEATURES	Direct Submission		
	source	Submitted (12-APR-2000) Division of Cytogenetics, National Institute of Agricultural Science and Technology, Seodun-dong, Suwon 441-707, Korea		
		Location/Qualifiers		
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		/product="NAC6"		
		/protein_id="AAK17057.1"		
		/db_xref="GT:13272280"		
		/translation="MSGGDQIQLPPGRFRPTDELMVHNLCRRCAGLPAPVPIAELI		
		DLYKPDFWOLPRMAYGEKEWYFFSPSRDPYNGSPRNKAATGSGTWTAKATGPKVSP		
		KPVATIKKALVVTYAGKAPKGKETNWIMHEYRLADVDRSARKNSLRDDWVLCRIVNKK		
		GGLEKPPAAVAAGMWSSGGVQRKPMVGNAAVSSPPQKPVVAGPAPFDLAAVDYD		
	RESULT 14	AX656219/c		
	LOCUS	AX656219 2000 bp DNA		
	DEFINITION	Sequence 6089 from Patent WO0300898.		
	ACCESSION	AX656219		
	KEYWORDS	GI:29159033		
	SOURCE	Oryza sativa		
	Query Match	2.7%; Score 48; DB 8; Length 300029;		
	Best Local Similarity 100.0%; Pred. No. 4_3e-14;	Matchers 0; Mismatches 0; Indels 0; Gaps 0;		
		Promoter		
		mRNA		
	Qy	30 AAATTAATTAATTCCAAATTATAATAGACGACTGGTCAAACA 77		
	Db	262872 AAATTAATTAATTCCAAATTATAATAGACGACTGGTCAAACA 262919		
	CDS	join(2151..2316,2416..2690,3552..4022)		
		/gene="NAC6"		
		/codon_start=1		
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		/protein_id="AAK17057.1"		
		/db_xref="GT:13272280"		
		/translation="MSGGDQIQLPPGRFRPTDELMVHNLCRRCAGLPAPVPIAELI		
		DLYKPDFWOLPRMAYGEKEWYFFSPSRDPYNGSPRNKAATGSGTWTAKATGPKVSP		
		KPVATIKKALVVTYAGKAPKGKETNWIMHEYRLADVDRSARKNSLRDDWVLCRIVNKK		
		GGLEKPPAAVAAGMWSSGGVQRKPMVGNAAVSSPPQKPVVAGPAPFDLAAVDYD		

RPSDSMPRLHDSSCSBQVLSPEFACEVQSQPKISEWERTPATVGPINPAASILDPG
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polyA_signal 4581. 4556
/Gene="NAC6"

ORIGIN

Query Match	2.5%	Score 45;	DB 8;	Length 4817;
Best Local Similarity	100.0%	Pred. No.	3.1e-12;	
Matches	45;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;

Qy 46 CAAATTTTAAATAAGCAGGAGGTCAACAGTACAAGTAAAAA 90
Db 446 CAAATTTTAAATAAGCAGGAGGTCAACAGTACAAGTAAAAA 402

Search completed: October 2, 2004, 13:18:15
Job time : 11071 secs

Result No.	Score	Query Match	Length	DB ID	Description
c 1	50	2.8	628	28	AQ686477 nbxb0072B
c 2	38	2.1	748	28	AQ686491 nbxb0032J
c 3	30	1.7	569	28	AQ72200 nbxb0027L
c 4	30	1.7	629	14	CA754682 BR0300040

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	50	2.8	628	28	AQ686477 nbxb0072B
c 2	38	2.1	748	28	AQ686491 nbxb0032J
c 3	30	1.7	569	28	AQ72200 nbxb0027L
c 4	30	1.7	629	14	CA754682 BR0300040

ALIGNMENTS

Title:	US-10-009-570-1	28	AQ510840 nbxb0094A
Perfect score:	1772	1.6	AQ510840 nbxb0094A
Sequence:	1 acttttagataataaaggtaag.....ctcttccttcgtgcaag	1.6	CG408907 nbxb0049B
	7682.315 Million cell updates/sec	2.8	AQ331226 nbxb0014I
		2.8	AQ860090 nbxb00210
		2.8	AQ863506 nbxb0015P
		2.8	AQ158100 nbxb0015P
		2.8	AQ420332 UG04F12 O
		2.8	BZ692356 SP_Ba001
		2.8	CC692659 OGTA120TH
		2.8	CC692657 CGTA120TC
		2.8	CG164014 PUAY17TD
		2.8	AQ258385 nbxb0021P
		2.8	BH7704404 OGBOG28TH
		2.8	BH776225 famb015f0
		2.8	CB663138 OSJNB0D0M
		2.8	AO914858 nbeb0030I
		2.8	AG025502 Oryza sat
		2.8	CC833513 ZMBB0018
		2.8	CC1323424 Kt71b08_Y
		2.8	BI450665 Kt73b08_Y
		2.8	AQ287509 nbxb0010K
		2.8	AQ872280 nbeb0047D
		2.8	AQ872280 nbeb0047D
		2.8	EZ786519 PUGDU05ID
		2.8	CC400206 PUBFS37TD
		2.8	CG371013 OGYA-S24TH
		2.8	CG916678 ZMBB0018
		2.8	AQ158754 nbxb0012G
		2.8	AZ126542 OSJNB0007
		2.8	CC710816 ZMBB0015
		2.8	BZ76519
		2.8	CC400206 PUBFS37TD
		2.8	BZ962486 PUGDU05TB
		2.8	AQ914858 nbeb0050I
		2.8	CC370652 PUBGK1CTD
		2.8	CC037205 3591_1_85
		2.8	EH78888 F2mb021f0
		2.8	CC019946 3591_1_17
		2.8	AQ510347 nbxb0095C
		2.8	CG286306 OG5AR0TC
		2.8	CG007640 2UADY94T

RESULT 1	AQ686477/c	628 bp	DNA linear	GSS 01-JUL-1999
LOCUS	nbxb0072B19r CUGI Rice BAC Library	Oryza sativa (japonica cultivar-group)		
DEFINITION	genomic clone nbxb0072B19r, genomic survey	cultivar-group		
SEQUENCE				
ACCESSION	AQ686477			
VERSION	AQ686477.1			
KEYWORDS	GSS			
SOURCE	Oryza sativa (japonica cultivar-group)			
ORGANISM	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	Liliopsida; Poales; Poaceae; Ehrhartodeae; Oryzae; Oryza;			
REFERENCE	1-1 (bases 1 to 628)			
AUTHORS	Wing, R.A. and Dean, R.A.			
TITLE	A BAC End Sequencing Framework to Sequence the Rice Genome			
JOURNAL	Unpublished (1998)			
COMMENT	Contact: Wing RA Clemson University Genomics Institute Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288 Fax: 864 656 4293 Email: rwing@clemson.edu Seq primer: GCAAAACGCTATGACCATG Class: BAC ends			

FEATURES High quality sequence stop: 384.
Location/Qualifiers 1..628

/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/strain="Japonica"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="nbbeb0032U14r"
/tissue_type="Leaf"
/lab_host="E. coli DH10B"
/clone_lib="CUGI Rice BAC Library (ECORI)"
/note="Vector: PBACIndigo; Site_1: ECORI; Site_2: EcoRI; lab host=E. coli DH10B"
/note="Rice is one of two most popular grains in the world. Half of the world population, especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from *Oryza sativa*, Nipponbare variety, using EcoRI as the cloning enzyme. The library contains 55,296 clones with an average insert size of 121 Kb providing approximately 15 haploid genome equivalents. The deep coverage allows the isolation of a particular sequence with a probability of 99.9 %. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/EST Resource Center (www.genome.clemson.edu)."

ORIGIN

Query Match	Score 2.8%; DB 28; Length 628;	Score 50%; DB 28; Length 628;	Score 100.0%; DB 28; Length 628;
Qy 7 GATAATAAGTAAAGTCACAGAAGAAAATAATAATTCCAAATTTTTT 56			
Db 485 GATAATAAGTAAAGTCACTACAGAAGAAAATAATAATTCCAAATTTT 436			

RESULT 2
AQ868991 LOCUS A0868991 748 bp DNA linear GSS 03-NOV-1999
DEFINITION nbbeb0032U14r CUGI Rice BAC Library (ECORI) *Oryza sativa* (japonica cultivar-group) Genomic Clone nbbeb0032U14r, genomic survey sequence.

ACCESSION VERSION AQ868991.1 GI:6219442
KEYWORDS SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viriplantae; Streptophytina; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartioideae; Orzeae; Oryza.
REFERENCE AUTHORS Wing,R.A. and Dean,R.A.
TITLE A BAC End Sequencing Framework to Sequence the Rice Genome
JOURNAL Unpublished (1998)
COMMENT Contact: Wing RA
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: TATAACGACTCATATAGGG
Class: BAC ends
High quality sequence stop: 316.

FEATURES source
source High quality sequence start: 34
High quality sequence stop: 416.
Location/Qualifiers 1..748

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/lab_host="E. coli DH10B"
/clone_lib="CUGI Rice BAC Library (ECORI)"
/note="Vector: PBACIndigo; Site_1: ECORI; Site_2: EcoRI; lab host=E. coli DH10B"
/note="Rice is the most important food crop in the world. Half of the world population, especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from *Oryza sativa*, Nipponbare variety, using EcoRI as the cloning enzyme. The library contains 55,296 clones with an average insert size of 121 Kb providing approximately 15 haploid genome equivalents. The deep coverage allows the isolation of a particular sequence with a probability of 99.9 %. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/EST Resource Center (www.genome.clemson.edu)."

ORIGIN

Query Match	Score 2.1%; DB 28; Length 748;	Score 38%; DB 38; Length 748;	Score 100.0%; DB 38; Length 748;
Qy 29 AAAATAATAATAATAATTCCAAATTTTTTAATAAGAGCGA 66			
Db 425 AAAATAATAATAATAATTCCAAATTTTTTAATAAGAGCGA 462			

RESULT 3
AQ272200 /C 569 bp DNA linear GSS 03-NOV-1998
LOCUS nbbeb0027L15F CUGI Rice BAC Library *Oryza sativa* (japonica cultivar group) genomic clone nbbeb0027L15F, genomic survey sequence.
DEFINITION AQ272200 GI:3825515
VERSION AQ272200.1
KEYWORDS GSS.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viriplantae; Streptophytina; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartioideae; Orzeae; Oryza.
REFERENCE 1 (bases 1 to 569)
AUTHORS Wing,R.A. and Dean,R.A.
TITLE A BAC End Sequencing Framework to Sequence the Rice Genome
JOURNAL Unpublished (1998)
COMMENT Contact: Wing RA
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: GGAAACGCTATGACCATG
Class: BAC ends
High quality sequence stop: 316.
Location/Qualifiers 1..569
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"

/strain="Japonica"
 /cultivar="Nipponbare"
 /db_xref="taxon:39947"
 /clone="nbxb0027L5F"
 /tissue_type="Leaf"
 /lab_host="E. coli DH10B"
 /clone_lib="CUGI Rice BAC Library"
 /note="Vector: pbeloBAC1; Site 1: HindIII; Site 2:
 HindIII: Rice is one of two most popular grains in the
 world. Half of the world population especially those
 inhabiting highly populated areas of the humid tropics
 and subtropics, rely on rice as their primary source of
 carbohydrate. Monocotyledonous rice is a diploid plant
 $(2n=24)$ with a haploid genome equivalent of 431 Mbp
 (Arumuganathan and Earle, 1991). The relatively small
 genome of rice, three times larger than that of
 Arabidopsis, makes it suitable for genomic studies. In
 order to facilitate positional cloning, physical mapping
 and genome sequencing of rice, we have constructed a BAC
 library from *Oryza sativa*, Nipponbare variety. The
 library contains 36,864 clones with an average insert size
 of 128.5 Kb providing 10.9 haploid genome equivalents. The
 deep coverage allows the isolation of a particular sequence
 with a probability of 99.9 %. Two high density filters,
 each containing 18,432 clones (doubly spotted), represent
 the whole library for colony screening."

ORIGIN

Query Match	Score	DB	Length	Source
Qy 29 AAATAAATATAATTCCAAATTCTTAA 58	1.7%	28	569	
Db 496 AAATAAATATAATTCCAAATTCTTAA 467	100.0%	222	0	

RESULT 4

Query Match	Score	DB	Length	Source
Qy 29 AAATAAATATAATTCCAAATTCTTAA 58	1.7%	28	569	
Db 496 AAATAAATATAATTCCAAATTCTTAA 467	100.0%	222	0	

Query Match 1.7% Score 30; DB 28; Length 569;
 Best Local Similarity 100.0%; Pred. No. 0.222; Indels 0; Gaps 0;
 Matches 30; Conservative 0; Mismatches 0; Insertions 0; Deletions 0;

DEFINITION EST 27-NOV-2002
 CULTIVAR GROUP: cDNA clone BR03004000_PLATE_E02_13_017.ab1 similar
 to No protein alignment, mRNA sequence.

ACCESSION CAT54682.1 GI:25798713

VERSION 1 (bases 1 to 629)

KEYWORDS EST.

ORGANISM *Oryza sativa* (japonica cultivar-group)
 Bacterial; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina;
 Spermatophytina; Magnoliophytina; Liliopsida; Poales; Poaceae;
 Ehrhartoidae; Oryzeae; Oryza.

REFERENCE Authors: Bonnett, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M., Ferrer, H., Kawauchi, S., McColough, A., Michalowski, C.B., Palacio, C., Scara, G., Wheeler, M., and Zepeda, G.R.
 Title: Functional Genomics of Plant Stress Tolerance
 Journal: Unpublished (2000)
 Contact: Mark Fredricksen
 Department of Plant Biology
 University of Illinois
 1201 W. Gregory Dr., Urbana, IL 61801, USA
 Tel: 217/255-473
 Email: bohnertlab@life.uiuc.edu.

Location/Qualifiers 1..629

FEATURES source

Query Match 1.7% Score 30; DB 14; Length 629;
 Best Local Similarity 100.0%; Pred. No. 0.2; Indels 0; Gaps 0;
 Matches 30; Conservative 0; Mismatches 0; Insertions 0; Deletions 0;

DEFINITION nbxb009A05r CUGI Rice BAC Library *Oryza sativa* (japonica cultivar-group) genomic clone nbxb009A05r, genomic survey sequence.

ACCESSION AQ510840

VERSION 1 (bases 1 to 537)

KEYWORDS GSS 04-MAY-1999

DEFINITION nbxb009A05r CUGI Rice BAC Library *Oryza sativa* (japonica cultivar-group) genomic clone nbxb009A05r, genomic survey sequence.

ORGANISM *Oryza sativa* (japonica cultivar-group)
 Bacterial; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina;
 Spermatophytina; Magnoliophytina; Liliopsida; Poales; Poaceae;
 Ehrhartoidae; Oryzeae; Oryza.

REFERENCE Authors: Wing, R.A. and Dean, R.A.
 Title: A BAC End Sequencing Framework to Sequence the Rice Genome
 Journal: Unpublished (1998)
 Contact: Wing, R.A.
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: rwing@clemson.edu

SEQ PRIMER: GGAAACAGCTATGACCATG

CSS: BAC ends

CLASS: High quality sequence start: 59
 High quality sequence stop: 437.

COMMENT Location/Qualifiers

1. 537

ORGANISM "Oryza sativa" (japonica cultivar-group)"

MOL TYPE: "Genomic DNA"

STRAIN: "Japonica"

CULTIVAR: "Nipponbare"

DB XREF: "Taxon:39947"

CLONE: "nbxb009A05r"

TISSUE: "Leaf"

LAB HOST: "E. coli DH10B"

CLONE LIB: "CUGI Rice BAC Library"

NOTE: "Vector: pbeloBAC1; Site 1: HindIII; Site 2: HindIII; Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant ($2n=24$) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from *Oryza sativa*, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation of a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."

ORIGIN

Query Match 1.6%; Score 29; DB 28; Length 537;
 Best Local Similarity 100.0%; Pred. No. 0.58;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 48 AATTTTTAAATAAGAGGAGTGGTCAAC 76
 Db 508 AATTTTTAAATAAGAGGAGTGGTCAAC 536

RESULT 6
 AQ510840/c LOCUS nxb009405r CUGI Rice BAC Library Oryza sativa (japonica cultivar group) genomic clone nbxb009405r, genomic survey sequence.
 ACCESSION AQ510840
 VERSION GSS
 SOURCE ORGANISM Oryza sativa (japonica cultivar-group)
 KEYWORDS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartioideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 331)
 AUTHORS Kim,C.M., Piao,H.L., Park,S.J., Chon,N.S., Je,B.I., Sun,B., Park,S.H., Park,J.Y., Lee,E.J., Kim,M.J., Lee,J.J., Nam,W.H., Eun,M.Y. and Han,C.D.

TITLE Rapid, Large-scale generation of Ds transposant lines and analysis of Ds loci in rice

JOURNAL Unpublished (2003)
 COMMENT Contact: Chang-deok Han
 DIVISION Division of Applied Life Science, PMBRC
 INSTITUTION Gyeongsang National University
 ADDRESS Gazwa-dong 900, Jinju 660-701, South Korea
 PHONE Tel: +82 55 751 6039
 FAX: +82 55 759 9363
 EMAIL: cdhan@iongae.gsnu.ac.kr
 LOCATION chromosome 4 clone OSJNBB0034G17

FEATURES source /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="genomic DNA"
 /cultivar="Dongjin"
 /db_xref="taxon:39947"
 /clone_lib="Ds insertion lines"

ORIGIN Query Match 1.6%; Score 28; DB 29; Length 331;
 Best Local Similarity 100.0%; Pred. No. 2.1%;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FEATURES source /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="genomic DNA"
 /strain="Nipponbare"
 /cultivar="Nipponbare"
 /db_xref="taxon:39947"
 /clone_type="leaf"
 /lab_host="E. coli DH10B"
 /clone_lib="CUGI Rice BAC Library"
 /note="Vector: pBeloBAC11; Site: HindIII; Site: 2;"
 /note="Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24), with a haploid genome equivalent of 431 Mb (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa. Nipponbare variety, The library contains 36,864 clones with an average insert size of 128.5 KB providing 10.9 haploid genome equivalents. The deep coverage allows the isolation of a particular sequence with a probability of 99.9%. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."

ORIGIN Query Match 1.6%; Score 29; DB 28; Length 537;
 Best Local Similarity 100.0%; Pred. No. 0.58;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
 CG408907/c LOCUS CG408907 DS insertion lines Oryza sativa (japonica cultivar-group)
 DEFINITION DS001 Ds insertion lines Oryza sativa (japonica cultivar-group). Genomic survey sequence.
 ACCESSION CG408907
 VERSION GSS
 KEYWORDS SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 KEYWORDS Butkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartioideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 331)
 AUTHORS Kim,C.M., Piao,H.L., Park,S.J., Chon,N.S., Je,B.I., Sun,B., Park,S.H., Park,J.Y., Lee,E.J., Kim,M.J., Lee,J.J., Nam,W.H., Eun,M.Y. and Han,C.D.

TITLE Rapid, Large-scale generation of Ds transposant lines and analysis of Ds loci in rice

JOURNAL Unpublished (2003)
 COMMENT Contact: Chang-deok Han
 DIVISION Division of Applied Life Science, PMBRC
 INSTITUTION Gyeongsang National University
 ADDRESS Gazwa-dong 900, Jinju 660-701, South Korea
 PHONE Tel: +82 55 751 6039
 FAX: +82 55 759 9363
 EMAIL: cdhan@iongae.gsnu.ac.kr
 LOCATION chromosome 4 clone OSJNBB0034G17

FEATURES source /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="genomic DNA"
 /cultivar="Dongjin"
 /db_xref="taxon:39947"
 /clone_lib="Ds insertion lines"

ORIGIN Query Match 1.6%; Score 28; DB 29; Length 331;
 Best Local Similarity 100.0%; Pred. No. 2.1%;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
 AQ331226/c LOCUS AQ331226 CUGI Rice BAC Library Oryza sativa (japonica cultivar-group) genomic clone nbxb0049E15r, genomic survey sequence.
 DEFINITION AQ331226

ACCESSION AQ331226
 VERSION GSS
 KEYWORDS SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 KEYWORDS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartioideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 409)
 AUTHORS Wing, R.A. and Dean, R.A.

TITLE A BAC End Sequencing Framework to Sequence the Rice Genome

JOURNAL Unpublished (1998)

COMMENT On Dec 15, 1999 this sequence version replaced g1:4123076. Contact: Wing RA.

Clemson University Genomics Institute
Clemson University
1100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: genomics@clemson.edu

Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: TAATACGACTATAGGG
Class: BAC ends
High Quality sequence start: 31

```

Seq primer: GCAAACTATGACCATG
Class: BAC ends
Location/Qualifiers "High quality sequence stop: 1.
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/organism="Orzya sativa (japonica cultivar-group)"
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/cione="nxb0049E15"
/tissue type="Leaf"
/lab_host="E. coli DH10B"
/cione lib="CUGI Rice BAC Library"
/note="Vector: pBeloBAC11; Site 1: HindIII; Site 2: HindIII; Rice is one of two most popular grains in world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mb (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. Order to facilitate positional cloning, physical map and genome sequencing of rice, we have constructed a library from Oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert of 128.5 Kb providing 10.9 haploid genome equivalent deep coverage allows the isolation of a particular sequence with a probability of 99.9 %. Two high density filters each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."

```

RIGGIN

Query Match 1.6%; Score 28; DB 28; Length 452;
 Best Local Similarity 100.0%; Pred. No. 1.7;

RESULT 10
AO863506_c
LOCUS
DEFINITION
nbeb021007f CUGI Rice BAC Library (ECORI) Oryza sativa (Japonica cultivar group) genomic clone nbeb021007f, Genomic survey

KEYWORDS	GSS; <i>Oryza sativa</i> (japonica cultivar-group); <i>Oryza sativa</i> (indica cultivar-group); Bokkenkato; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytina; Magnoliopsida; Liliopsida; Poales; Poaceae; Ehrhartioideae; Oryzeae; <i>Oryza</i> .
SOURCE ORGANISM	

REFERENCE
1 (bases 1 to 46)
Wing R.A. and Dean, R.A.
AUTHORS
A BAC End Sequencing Framework to Sequence the Rice Genome
TITLE
Unpublished (1998)
JOURNAL
COMMENT
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293

FEATURES	source	Seq primer: GGAAACAGGTTATGCCATG Class: BAC ends High quality sequence start: 28 High quality sequence stop: 438. Location/Qualifiers
1. '466		/organism="Oryza sativa (japonica cultivar-group)"
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/clone="nbeb002100f"		/tissue type="Leaf"
/lab_hofo="E. coli DH10B"		/clone lib="CUGI Rice BAC Library"
/note="Vector: pBACIndigo; Site 1: EcoRI; Site 2: BcoRI; Rice is the most important food crop in the world. Half of the world population, especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrates. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa Nipponbare variety using BcoRI as the cloning enzyme. The library contains 55,296 clones with an average insert size of 121 Kb providing approximately 15 haploid genome equivalents. The deep coverage allows the isolation of a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/EST Resource Center (www.genome.clemson.edu)."		
ORIGIN		
Query Match	Qy	29 AAAATAATAATTCAAATTTTT 56
Best Local Similarity	1.6%	Score 28; DB 28; Length 46;
Matches	28	Conservative 0; Mismatches 0; Gaps 0;
Db	264	AAAATAATAATTCAAATTTTT 237
RESULT 11		
LOCUS	AQ258100	623 bp
DEFINITION	nxbx0019p11r CUGI Rice BAC Library	DNA linear
ORGANISM	Oryza sativa (japonica cultivar-group)	GSS 23-OCT-1998
COMMENT	genomic clone nbxb0019p11r, genomic survey sequence.	
REFERENCE	AQ258100	G1:3782582
AUTHORS	Wing R.A. and Dean,R.A.	
TITLE	A BAC End Sequencing Framework to Sequence the Rice Genome	
JOURNAL	Unpublished (1998)	
COMMENT	Contact: Wing RA	
REFERENCE	100 Jordan Hall, Clemson, SC 29634, USA	
AUTHORS	Clemson University Genomics Institute	
JOURNAL	Tel: 864 656 7288	
COMMENT	Fax: 864 656 4293	
FEATURES	Email: rwing@clemson.edu	
source		

FEATURES	source	Seq primer: GGAAACAGGTTATGCCATG Class: BAC ends High quality sequence stop: 286. Location/Qualifiers	
1. '623		/organism="Oryza sativa (japonica cultivar-group)"	
/mol_type="genomic DNA"		/strain="Japonica"	
/db_xref="Nipponbare"		/clone="nbxb0019p11r"	
/tissue type="Leaf"		/lab_hofo="E. coli DH10B"	
/clone lib="CUGI Rice BAC Library"		/note="Vector: pBeloBAC11; Site 1: HindIII; Site 2: HindIII; Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrates. Monocotyledonous rice is a diploid plant (2n=14) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa Nipponbare variety using BcoRI as the cloning enzyme. The library contains 36,864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation of a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."	
ORIGIN			
Query Match	Qy	49 ATTTTTTAATAAGCAGTAGTCAAC 76	
Best Local Similarity	1.6%	Score 28; DB 28; Length 623;	
Matches	28	Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Db	283	ATTTTTTAATAAGCAGTAGTCAAC 256	
RESULT 12			
LOCUS	BM420232	652 bp mRNA linear	
DEFINITION	U004f12 Oryza sativa mature leaf library induced by M.grisea Oryza sativa cDNA clone U004f12, mRNA sequence.	EST 28-JAN-2002	
ACCESSION	BM420232		
VERSION	BM420232.1	GI:18387034	
KEYWORDS			
ORGANISM	Oryza sativa		
SOURCE	Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Spermatophytina; Magnoliophytina; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.		
COMMENT	Contact: Haitao Dong, Debao Li Bioinformatics and Gene Network Research Group Zhejiang University Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China		
REFERENCE	Dong,H.T., Li,D.B., Zhuang,X.F., Dai,C.G., Sun,L.X., Pei,Y.X., Wu,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K. and Lou,Y.C.		
AUTHORS	A Gene Expression Screen in Oryza sativa		
TITLE	Unpublished (2001)		
JOURNAL			
COMMENT	Contact: Haitao Dong, Debao Li Bioinformatics and Gene Network Research Group Zhejiang University Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China		
REFERENCE	Wing R.A. and Dean,R.A.		
AUTHORS	A BAC End Sequencing Framework to Sequence the Rice Genome		
JOURNAL	Unpublished (1998)		
COMMENT	Contact: Wing RA		
REFERENCE	100 Jordan Hall, Clemson, SC 29634, USA		
AUTHORS	Clemson University Genomics Institute		
JOURNAL	Tel: 864 656 7288		
COMMENT	Fax: 864 656 4293		
FEATURES	Email: rwing@clemson.edu		
source			

/mol_type="mRNA"						
/db_xref="Taxon:4530"						
/clone="U004F12"						
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Query Match Similarity 1.6%; Score 28; DB 12; Length 652; Best Local Similarity 100.0%; Pred. No. 1.; Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
Qy 57 AATAAGCAGGTGTCATACAGTACAAG 94						
Db 542 AATAAGCAGGTGTCATACAGTACAAG 569						
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LOCUS	SP_Ba0019009.f	SP_Ba0019009.5	Ba	Sorghum propinquum	genomic clone	
DEFINITION	SP_Ba0019009_5	_				
GENOMIC SURVEY SEQUENCE						
REFERENCE	BZ692356					
AUTHORS						
KEYWORDS						
SOURCE						
ORGANISM						
Sorghum propinquum						
Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Spermatophytina; Magnoliophytina; Liliopsida; Poales; Poaceae; PACCD clade; Panicoidea; Andropogoneae; Zea.						
1 (bases 1 to 783)						
COMMENT	Cathy Whitelaw					
ACCESION	BZ692356					
VERSION	GI:28384160					
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ORGANISM						
Sorghum propinquum						
Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Spermatophytina; Magnoliophytina; Liliopsida; Poales; Poaceae; PACCD clade; Panicoidea; Andropogoneae; Zea.						
1 (bases 1 to 694)						
COMMENT	Cathy Whitelaw					
Wing, R., Yu, Y., Kim, H.R., Collura, K., Pries, G., Currie, J., Soderlund, C. and Haefield, J.						
SEQUENCING	http://genome.arizona.edu/stc/sorghum					
CONTACT	Rod Wing					
UNPUBLISHED	(2003)					
JOURNAL	Arizona Genomics Institute					
COMMENT	University Of Arizona Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ 85724-0088, USA					
TELEPHONE	520 626 3967					
FAX	520 621 9288					
EMAIL	http://genome.arizona.edu					
PCR PRIMERS						
FORWARD: atc agc ggc cgc gat cc						
BACKWARD: gta aaa cga cgg cca gtg						
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1 (bases 1 to 787)						
COMMENT	Cathy Whitelaw					
ACCESION	CC692657					
VERSION	GI:32097433					
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COMMENT	Cathy Whitelaw					
ACCESION	CC692657					
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1 (bases 1 to 787)						
COMMENT	Cathy Whitelaw					
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COMMENT	Cathy Whitelaw					
ACCESION	CC692657					
VERSION	GI:32097433					
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1 (bases 1 to 787)						
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Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Spermatophytina; Magnoliophytina; Liliopsida; Poales; Poaceae; PACCD clade; Panicoidea; Andropogoneae; Zea.						
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COMMENT	Cathy Whitelaw					
ACCESION	CC692657					
VERSION	GI:32097433					
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1 (bases 1 to 787)						
COMMENT	Cathy Whitelaw					
ACCESION	CC692657					
VERSION	GI:32097433					
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1 (bases 1 to 787)						
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ACCESION	CC692657					
VERSION	GI:32097433					
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Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Spermatophytina; Magnoliophytina; Liliopsida; Poales; Poaceae; PACCD clade; Panicoidea; Andropogoneae; Zea.						
1 (bases 1 to 787)						
COMMENT	Cathy Whitelaw					
ACCESION	CC692657					
VERSION	GI:32097433					
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SOURCE						
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Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Spermatophytina; Magnoliophytina; Liliopsida; Poales; Poaceae; PACCD clade; Panicoidea; Andropogoneae; Zea.						
1 (bases 1 to 787)						
COMMENT	Cathy Whitelaw					
ACCESION	CC692657					
VERSION	GI:32097433					
FEATURES						
SOURCE						
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Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Spermatophytina; Magnoliophytina; Liliopsida; Poales; Poaceae; PACCD clade; Panicoidea; Andropogoneae; Zea.						
1 (bases 1 to 787)						
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ACCESION	CC692657					
VERSION	GI:32097433					
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1 (bases 1 to 787)						
COMMENT	Cathy Whitelaw					
ACCESION	CC692657					
VERSION	GI:32097433					
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SOURCE						
ORGANISM						
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Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Spermatophytina; Magnoliophytina; Liliopsida; Poales; Poaceae; PACCD clade; Panicoidea; Andropogoneae; Zea.						
1 (bases 1 to 787)						
COMMENT	Cathy Whitelaw					
ACCESION	CC692657					
VERSION	GI:32097433					
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1 (bases 1 to 787)						
COMMENT	Cathy Whitelaw					
ACCESION	CC692657					
VERSION	GI:32097433					
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Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Spermatophytina; Magnoliophytina; Liliopsida; Poales; Poaceae; PACCD clade; Panicoidea; Andropogoneae; Zea.						
1 (bases 1 to 787)						
COMMENT	Cathy Whitelaw					
ACCESION	CC692657					
VERSION	GI:32097433					
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Sorghum propinquum						
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1 (bases 1 to 787)						
COMMENT	Cathy Whitelaw					
ACCESION	CC692657					
VERSION	GI:32097433					
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1 (bases 1 to 787)						
COMMENT	Cathy Whitelaw					
ACCESION	CC692657					
VERSION	GI:32097433					
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Sorghum propinquum						
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1 (bases 1 to 787)						
COMMENT	Cathy Whitelaw					
ACCESION	CC692657					
VERSION	GI:32097433					
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SOURCE						
ORGANISM						
Sorghum propinquum						
Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Spermatophytina; Magnoliophytina; Liliopsida; Poales; Poaceae; PACCD clade; Panicoidea; Andropogoneae; Zea.						
1 (bases 1 to 787)						
COMMENT	Cathy Whitelaw					
ACCESION	CC692657					
VERSION	GI:32097433					
FEATURES						
SOURCE						
ORGANISM						
Sorghum propinquum						
Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Spermatophytina; Magnoliophytina; Liliopsida; Poales; Poaceae; PACCD clade; Panicoidea; Andropogoneae; Zea.						
1 (bases 1 to 787)						
COMMENT	Cathy Whitelaw					
ACCESION	CC692657					
VERSION	GI:32097433					
FEATURES						
SOURCE						
ORGANISM						
Sorghum propinquum						
Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Spermatophytina; Magnoliophytina; Liliopsida; Poales; Poaceae; PACCD clade; Panicoidea; Andropogoneae; Zea.						
1 (bases 1 to 787)						
COMMENT	Cathy Whitelaw					
ACCESION	CC692657					
VERSION	GI:32097433					
FEATURES						
SOURCE						
ORGANISM						
Sorghum propinquum						
Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Spermatophytina; Magnoliophytina; Liliopsida; Poales; Poaceae; PACCD clade; Panicoidea; Andropogoneae; Zea.						
1 (bases 1 to 787)						

Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.

FEATURES
source Location/Qualifiers
 1. .787
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 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone_id="ZMMBMA0389c15"
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 /note="Vector: pBCSK; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN
Query Match 1.6%; Score 28; DB 29; Length 787;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 48 AATTTTTTAAAGCAGTGTCAA 75
Db 495 AATTTTTTAAAGCAGTGTCAA 468

Search completed: October 2, 2004, 15:13:13
Job time : 6892 secs